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RESULT 38
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Query Match 53.2%; Score 1284.5; DB 2; Best Local Similarity 59.4%; Pred. No. 1.1e-64; Matches 280; Conservative 30; Mismatches 68;
                                            Polynucleotides encoding the L and H chains of human anti-HBs Ab are given in AAQ49943-Q49944. The Ab can be easily produced in large quantities for therapeutic use. (Updated on 25-MAR-2003 to correct PN field.)
                             Sequence 459 AA;
                                                                                Disclosure; Fig 6-8; 46pp; Japanese.
                                                                                              Human anti-hepatitis B surface antigen antibody gene - can produce L and H chains of the antibody in large quantity.
                                                                                                                     WPI; 1993-336913/42.
N-PSDB; AAQ49944.
                                                                                                                                            Kurihara
                                                                                                                                                                         30-MAR-1992;
                                                                                                                                                                                       30-MAR-1993;
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                              Antibody; Ab; light; heavy; chain; hepatitis B; HB; surface antigen.
                                                                                                                                                                                                                                                                                                            Human anti-HBs heavy chain
                                                                                                                                                                                                                                                                                                                            25-MAR-2003
29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                 AAR42066 standard;
                                                                                                                                                                                                      14-OCT-1993
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                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                            /label= sig_peptide
10. .459
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06-SEP-1996
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RESULT 39
AAW05829
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                Humanised 1D10 antibody heavy chain
                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2003
27-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW05829;
                                                                                                                        Region
                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALASGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRFDSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGVV--QPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFYADSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNKVVLGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKIL---GNQGSFL--TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                         /label= CDR1
50. .65
/label= CDR2
98. .105
/label= CDR3
                        215. .229
/label= Hinge
230. .339
/label= CH2
                                                                  /label= CH1
215. .229
340. .446
/label= CH3
                                                                                                                                                                             /label= Variable_domain
31. .35
                                                                                                                                                                                                                    Location/Qualifiers
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The humanised 1D10 antibody heavy chain (AAW05829) includes a variable region (see also AAW05823) consisting of human R3.5HG heavy chain variable region framework and complementarity determining regions from the murine 1D10 antibody specific for a 28/32 kDa antigen found on the surface of malignant B-cells. It can be coexpressed with humanised 1D10 light chain (see also AAW05828) in mammalian host cells. Bispecific antibodies can be constructed that include a first binding fragment comprising humanised M211 heavy and light chain variable regions (see also AAW05826, AAW05830), and a second binding fragment comprising humanised M211 heavy and light chain variable regions. Such antibodies are reactive with both T or NK cells and malignant B cells, and have therapeutic and diagnostic applns. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bi-specific antibody reactive with both T or NK cells and malignant cells - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia, lymphoma and myeloma.
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IOWA IMMUNOTHERAPY INVESTIGATORS.
                   KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                  YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                    TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                   QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                                                                                                                                                                                                                                                                                                                                   VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHFTPAVL
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                  CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                    QDSG-----TWTCTVLQNQKKVEFKIDIVFCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                     LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----QLEL
                                                                                                                                                                                                                                                                                                                                                                                                        KDTSKNQVSLKLNSLTAADTAVYYC-------ARNDRYAMDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                       --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1282.5; DB
; Pred. No. 1.4e-64;
25; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tso JY;
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445
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RESULT 40 ABJ37106

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                      soluble domains, in which an N-terminus of a soluble domain of a biologically active protein is linked to a C-terminus of an identical soluble domain or a different soluble domain of a biologically active protein. The methods and compositions of the present invention are use for the diagnosis and treatment of disorders associated with dimeric protein or its glycosylated form, such as inflammation, especiated to the protein or the glycosylated form, such as inflammation of the protein or its glycosylated form, such as inflammation of the protein or its glycosylated form, such as inflammation of the protein or the glycosylated form such as inflammation.
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New concatameric protein having two soluble domains, useful for diagnosing and treating disorders associated with the dimeric its glycosylated form, such as inflammation, septicemia, rheur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic; immunomodulator; concatameric protein; sol dimeric protein; inflammation; septicaemia; cytotoxicity; rheumatoid arthritis; cachexia; inflammation; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis and cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel concatameric protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003010202-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiinflammatory; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Concatameric
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                                                                                                                                                                                                                                                                                                 Local Similarity
les 272; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              invention
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DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                      KIKHLKTDDODIYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
                                                                                                                                                                                                                                    DDIKWEKTSDKKKIAQFRKEKE-----TFKEKDTYKLFK-----NGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 171-174; 211pp;
                                            SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                              FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                        CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
                                                                                                                                       LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----
                                                                                                                                                                                                     IIKNLKIEDSDTYICEVEDOK-EEVOLLVFGLTANSDTHLLQGO----
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                                                                                                                                                                                                                                                               The invention relates to a novel concatameric protein comprising two soluble domains, in which an N-terminus of a soluble domain of a biologically active protein is linked to a C-terminus of an identical soluble domain or a different soluble domain of a biologically active protein. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with dimeric protein or its glycosylated form, such as inflammation, septicaemia, cytotoxicity, rheumatoid arthritis, cachexia and other inflammation related diseases. This sequence represents the human concatameric protein
                                                                                                                                                                                             Sequence
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                                                                                                New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                           Hanai N,
                                                                                                                                                                                                                                                                                                               cancer.
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The present invention describes a monoclonal antibody which can reac specifically with ganglioside GD3. The antibody and its derivatives useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplifica of the invention

exemplification

are

Claim

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Page 175-179;

183pp;

Japanese.

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RESULT 43
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                                                                                                                                                  Key
Peptide
                                               WO200162801-A2
                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                   Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
                                                                                                                                                                                                                                                                                                                     Humanised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYSDSVKGRFTIS-
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                                                                                                                                                                                                                                                                                                                     monoclonal
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                                                                                                                      1. .19
/label= Signal_peptide
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.1%; Score 1282; DB 4; 57.5%; Pred. No. 2e-64;
                                                                                                                                                                                                                                                                                                                   antibody Hu266, heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 582;
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Best Local S
Matches 282
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08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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nes 282; Conserv
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NHYTQKSLSLSPG
                                                                                                                          LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                                                                                                                 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                                                               CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                                                                                                         ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTTLTLESPFGSSPSVQCRSPRGKNIQGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 AA;
                                               PSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                                                SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                                            CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                    AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
                                                                                                                                                                                                                                                                                                                   ----KTLSVS-----TWT
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2000US-0254498P
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                                                                                                                                                                                                                                                                                                                                                -----ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.0%; Score 1280.5; DB 4; Length 57.2%; Pred. No. 1.9e-64; tive 30; Mismatches 86; Indels
                  431
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KW fusic
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FT Regi
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                  A polypeptide (AAW11639) comprises a leader sequence, RF-1 heavy chain variable region (see also AAW11639), and human gamma 1 constant region. RF1 is a human monoclonal antibody (hMAb) specific for the fusion protein of respiratory syncytial virus (RSV). The polypeptide can be produced in eukaryotic host (e.g. CHO) cells transfected with vector NEOSPLA
                                                                                                                                                                                           Human monoclonal antibody specific for respiratory syncytial virus protein - used for the prevention and treatment of RSV infection.
                                                                                                                                                                                                                                                                                                                              Brams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1996;
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                                                                                                                                                       Example
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                                                                                                                                                  9b-c; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US010070
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/note= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR2
/note= "complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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'note= "framework
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Best Local S
Matches 282
                                                                   Homo sapiens.
Synthetic.
Chimeric.
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                                                                                                                                                  Stroke; neurological disease; neurodegeneration; brain injury; spinal cord injury; chronic disease; halbheimer's disease; tauopathy; fronto-temporal dementia; peripheral neuropathy; arkinson's disease; Huntington's disease; multiple sclerosis; mouse; human; anti-MAG;
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                                                                                                                                                                                                                                                                                                       standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
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Pred. No. 2e-64;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              administering a myelin-associated glycoprotein (MAG) antagonist or anti-MAG antibody, including altered antibodies or their functional fragment. The MAG antagonist or anti-MAG antibodies or their functional fragments are useful in preparing a medicament for treating or preventing stroke and other neurological diseases, or for inhibiting neurodegeneration and/or promoting functional recovery in a human patient suffering or at risk of developing stroke or other neurological disease, such as stroke, traumatic brain injury and spinal cord injury, chronic disease including Alzheimer's disease, fronto-temporal dementias (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease and multiple sclerosis. The present amino acid sequence represents the mouse/human chimeric anti-MAG antibody heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stroke and other neurological diseases in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or preventing stroke and neurological diseases, e.g. Alzheimer's multiple sclerosis or Parkinson's disease, comprises ering a myelin-associated glycoprotein (MAG) antagonist or anti-
                                                     GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
                                                                                                                   NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELIKNQVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                    DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
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                                                                                                                                                                 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                                 TKVD----KKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVV
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                                                                                                                                                                                                                                                                                                                                   -KTLSVS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates to a new method of treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                   ---QLELQDSG------
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AAW88464
AAW88464
ID AAW88
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CC 
                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic therapy to reduce risk of recurrence.
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lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody 4B5 heavy chain variable region
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     476
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Matches 280; Query Match Best Local

Similarity

56.9%;

Conservative

27;

Score 1280; DB 2; Pred. No. 2.1e-64; 7; Mismatches 91;

Length 476; Indels

94;

Gaps

12;

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                                                                                                                                                                                                                                                                                                                                                          heavy chain; anti-OD145; CD145-antibody complex; 3D structure; three dimensional structure; drug design; drug discovery; activated T cell; CD40 interaction; T cell dependent immune response; agonist; antagonist; immune response; inflammatory response; autoimmune disease; allergy; inhibitor response; organ graft rejection; B cell cancer; Alzheimer's disease; multiple sclerosis; antiinflammatory; immunosuppressive; antiallergic; cytostatic; dermatological; antiasthmatic; noctropic; neuroprotective; antiarteriosclerotic; antiarteriosclerotic; antiviral; antidabetic; cardiant; antischaemic; vasodilator; antirheumatic; antiarthritic; antipsoriatic; immunomodulator; antibody; complementarity determining region; CDR; protein co-ordinate data.
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Binding-site
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                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                   Homo
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(first entry)
/note=
                                                             31. .35
/label= CDR1
                                                                                                                                                                                  Location/Qualifiers
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                      "Complementarity determining region
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Crystal comprising a CD154 polypeptide complexed with an anti-CD154 antibody, or its antigen binding fragment, useful for designing drugs the treatment of an autoimmune disease, an allergy, multiple sclerosis and Alzheimer's disease.
                                                                                                                                                  01-SEP-2000;
16-MAR-2001;
                                                                     WPI; 2002-329760/36.
                                                                                                                                                                                           31-AUG-2001; 2001WO-US027352
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                                                                                              M, Hsu Y,
                                                                                                                                                    2000US-0229933P
2001US-0276452P
                                                                                                                                                                                                                                                                                    /note= "Complementarity determining 102. .103
                                                                                                                                                                                                                                                                          /note= "Binds to CD145 (AAM49202)"
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Example 1; Fig 8; 470pp; English.

for

The invention relates to a crystal comprising a CD145 polypeptide in CC complex with an anti-CD45 antibody or its antigen-binding fragment, and CC the structure coordinates of such a crystal. In particular, the crystal CC comprises human CD145 (AAM49202) and a humanised version of the murine CC CD401, gp39, T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type II CC membrane glycoprotein which is transiently expressed on activated T CC cells. It interacts with CD40 which is expressed on activated T CC cells. This CD40:CD145 interaction is required for T cell-dependent CC macrophages, dendritic cells, fibroblasts and activated endothelial CC cells. This CD40:CD145 interaction is required for T cell-dependent CC production by macrophages. No mediates many of the pro-inflammatory CC production by macrophages. No mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the pro-inflammatory Conditions. The crystal structure of the invention can be used to determine the three dimensional structure of the invention can be used to determine the three dimensional structure of the CD45 antibody complex, and thereby provide information CC constants and antagonists which modulate three dimensional structure of the compounds may be used in the treatment of an unwanted immune cc allergy, an inhibitor response to a therapeutic agent, rejection of a constant of the c psoriasis, atopic dermaticis, systemic scriver, training myeloma and fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma and cachexia. Sequences AAM49203 and AAM49204 represent, respectively, the heavy and light chains of the humanised version of the murine monocine.

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RESULT 48
AAY30201
ID AAY30
XX AAY30
XX 17-OC
DT 117-OC
DT 117-OC
DT 01-NC
XX Heavy
XX Heavy
XX Colla
XW Toolla
XW Toolla
XW Toolla
XX Toolla
XX Toolla
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XX LORIN
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Aruffo
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                                                                                                                                                                                       26-AUG-1999.
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                                                                                                                                                                                                                                                                                   Chimeric.
                                                                                                                                                                                                                                                                                                                                                                             transplantation.
                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain variable region; chimeric antibody; anti-CD40 antibody; chi220; humoral immune response; T cell dependent antigen; collagen induced archivitis; transplant induced rejection; T cell_mediated disorder; autoimmune disease; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain
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01-NOV-1999
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Hollenbaugh D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of chimeric anti-CD40 antibody chi220
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Pred. No. 2.1e-64;
1; Mismatches 74;
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                             Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagument; prevention; cell proliferation; immune system disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseared transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases, and transplantation. (Updated on 17-OCT-2003 standardise OS field)
                                                                                                        25-APR-2000
                                                                                                                                                                 AAY44721
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                                                                                                                                                                                                                                                                                                                 REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS
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                                                                                                                                                                                                                                                                                                                                                                                       VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGNFP-----LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKKPGETVRISCKAS---GYAFTTTGMQWVQEMPGKG---LKWIGWINTHSGVPKYVEDF
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                                                                                                                                                                                                                                          FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Homo sapiens

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Immune system molecules used of disorders associated with

in the diagnosis, treatment and prevention the immune system and cell proliferation.

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Matches 278
                                                     neuroprotective; hinge region; immunoglobulin heavy CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; malignant condition; B-cell disorder; melanoma; card
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is an immune system molecule, ISMO-2 from an Incyte clone 2849752 isolated from the human breast tumour cDNA library (BRSTTUT13). This sequence is expressed in several libraries, generally those associated with cancer, cell proliferation, immune response or trauma. It shows homology to vertebrate immunogloblin gamma heavy-chain. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation
Unidentified
                                                                                                                 antiarthritic;
                                                                                                                               Binding domain;
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                                                                                                                                                                                         15-JAN-2004
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                          type I diabetes
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                                          rheumatoid arthritis; myasthenia
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                                                                                                         immunoglobulin; fusion protein; immunosuppressive; antidiabetic;
                        ritis; myasthenia gravis; Grave's disease; mellitus; multiple sclerosis; autoimmune disease
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US2003118592-A1

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Query Match
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Matches 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hinge region polypeptide comprises: a wild-type human IgGi immunoglobulin hinge region polypeptide; a mutated human IgGI immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgGI immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgGI immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgGI immunoglobulin hinge region polypeptide contains no more than one
                                                                                                                                                                                                                                                                        Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
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17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 344; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a binding domain-immunoglobulin fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENECRAFT INC
    _
                                                                                                                                      Similarity
MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayden-Ledbetter MS,
                                                                                                                                  53.0%;
                                                                                   33;
                                                                                        Score 1279; DE Pred. No. 2.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson
                                                                                                                             .5e-64;
                                                                                                                                                                                DB 7;
                                                                                                                                                                       Length 492;
                                                                                            Indels
                                                                                            96;
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                                                                                   Gaps
    60
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밁 Ś

19

MSRGVD----IVL-----TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS---

62

The present invention describes an antibody, which can react specifically with ganglioside GD2, and is transplanted with a human type complementation-determining domain (CDR), or its fragments. The antibody

Example 3; Page 111-114; 123pp; Japanese

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RESULT 51
AAB81972
ID AAB81
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                                                                         Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumors, has low antigenicity, little side effects but potent activity in cancer.
                                                                                                                                            WPI; 2001-266163/27.
                                                                                                                                                                      Hanai N,
                                                                                                                                                                                                                                                 29-SEP-2000; 2000WO-JP006773
                                                                                                                                                                                                                                                                                                     WO200123573-A1
                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                   Ganglioside;
                                                                                                                                                                                                                                                                                                                                                                                             Ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB81972 standard;
                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                       30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                       mouse; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYCA-----RIHPDYWGQGVMVTVSSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVHWIROPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGTKLEIKRGGGGSGGGGGGGGGGQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVLHQDWLNGXEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTCTVLQNQKKVEFK-----IDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVQ-CRSPRGKNIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
                                                                                                                                                                    Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                            GD2 specific antibody related protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   GD2; complementation determining region; CDR; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
                                                                                                                                                                                                                        99JP-00278290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 581 AA
                                                                                                                                                                      Nakamura K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                                                                                                                                                                      Niwa R;
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Best Local Similarity
17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                Binding domain; immunoglobulin; fusion protein; cytostatic; antiatrhritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective, hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fix malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease;
                                                                                                                                                                                                                                                                                                                         Binding domain-immunoglobulin fusion protein-associated protein
                                                                                                                                                                                                                                                                                                                                                           15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                       ADD25784 standard;
                                                                                                                         US2003118592-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 particularly cancer the exemplification
                                                           25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-
                                                                                                                                                                                   diabetes mellitus; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQLDETCAEAQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGSSPSVQCRSPRGKNIQGG------KTLSVS------QLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDNSKNOVFLKMSSLTAADTAVYYCAKRSDDYSWFAY------WGQGTLVTVSSA 119
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are useful in diagnosis and therapy of tumours, diagnosis. The present sequence is a protein used of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                       543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1278.5;
Pred. No. 3.1e.
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                 sclerosis; autoimmune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81;
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                                                                                                                                                                                                                               fixation;
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New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                          Disclosure; SEQ ID NO 345; 157pp;
                                                                                                                                                                                                                                                          (GENE-) GENECRAFT INC
                                                                                                                                                                                                                                                Hayden-Ledbetter MS,
                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                Thompson
                                                                                                                                                                                                                                                PA
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CC comprising a binding domain polypeptide, an immunoglobulin heavy chain CC immunoglobulin hinge region polypeptide, and an immunoglobulin heavy chain CC CH2 constant region polypeptide that is fused to the hinge region come polypeptide, and an immunoglobulin heavy chain CC polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, derived from (a) having 3 or more cysteine residues; where the first cysteine residues; contains 2 cysteine residues, where the first cysteine residues contains 2 cysteine residues, where the first cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more than one (cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one (cysteine residues. The binding domain immunoglobulin hinge region polypeptide contains (construct cysteine residues) and a mutated human IgG1 immunoglobulin fusion protein is constructed of human IgG1 immunoglobulin fusion protein is constructed of mutated polypeptide contains (constructed cysteoxicity (ADCC) and complement fixation. The binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polymelectide with a recombinant expression construct comprising the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a subject having or suspected of having a malignant condition or a B-cell disorder. e.g. melanoma, carcinoma or sarcoma, reumatoid arthritis, multiple selection of the sequence in the printed specification by their SQQ ID condition or a broad to demain salve and is al The invention relates to a binding domain-immunoglobulin fusion protein 8

밁 Ś 밁 Ś 밁 Query Match Local Similarity mes 279; Conserv 152 19 19 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60 SVQ-CRSPRGKNIQ------GGKT--GSGTKLEIKRGGGGSGGGGGGGGGQQQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD ILGNOGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE-------GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120 Conservative 52.9%; 33; Score 1277; DB 7; Pred. No. 3.6e-64; 3; Mismatches 92 TOSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS------ EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP Length 543; Indels ---LSVSQLELQDSGT 181 96; Gaps 151 62

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RESULT 53
ABR39847
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          The invention relates to an anti-Abeta (amyloid-beta peptide) antibody 266. The antibodies are useful for treating and preventing conditions associated with the Abeta peptide, such as Alzhaimer's disease, Down syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in humans; for determining whether a human subject will respond to treatment using humanized antibodies against Abeta; for treating, preventing and reversing cognitive decline in clinical or pre-clinical Alzhaimer's disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting formation of amyloid plaques of the effects of toxic soluble Abeta species in humans. Treatment of the patients with antibody will inhibit or prevent cognitive decline typically associated with disease
 progression
                                                                                                                                                                                    Disclosure; Fig 6; 82pp; English.
                                                                                                                                                                                                                           New antibodies comprising a heavy chain and a light chain complementarity determining regions from antibody 266, for treating and preventing conditions associated with the A beta peptide, e.g. Alzheimer's disease
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Pred. No. 3.6e-64;
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Matches 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 461 AA;
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   02-APR-2003
                                 AAE33444;
                                                             AAE33444 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS--
                                                                                                                                                             NHYTOKSLSLSPG
                                                                                                                                                                                                                      PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                                                                                                                                                                   LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
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                                                                                                                                          NHYTOKSLSLSPG
                                                                                                                                                                                                      PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
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   (first entry)
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                                                             protein;
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Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 80-82; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant anti-EpCAM antibody having an amino acid sequence defining an immunoglobulin light or heavy chain framework region, useful for the diagnosis, prognosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-2001;
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SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG---
                                        PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDTAVEWESNGQPENNYKTTPPVLDSDG
                                                                                              EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                  THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMXVDGV
                                                                                                                                                   THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                     TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                                                 --QLELQDSG---
                                                                                                                                                                                                                                            TSVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                     QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS
                                                                                                                                                                                                                                                                                                                        DQGNFP------LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                         PREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG
                                                                              EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                FKGRFAFSLETSTSTAFLQINNLRSEDTATYFC-----VRFISKG-----DYWGQG
                                                                                                                                                                                                                                                                                                                                                      KPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTYADD------
                                                                                                                                                                                                                                                                                                                                                                               KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLW
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57.7%;
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Pred. No. 4.6e
29; Mismatches
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RESULT 56
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                                                       Matches
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                                                                                                                                  This is the amino acid sequence of a single chain antibody (Sab), termed $T94Sab1, comprising an scFv derived from murine monoclonal antibody $T4 (see AAW8602) and the human gl constant region. CDNA (see AAV8021) encoding the Sab has been inserted into vector pCIneo to allow expression in mammalian cells. The trophoblast cell surface antigen defined by $T4 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or pOI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage
                                                                                                            Sequence 595
                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1B; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                        New vector encoding a tumour interacting protein for treating cancer contains a desired nucleotide sequence and/or protein which recognise tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kingsman
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20-JUN-1997;
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                            TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aracting protein; cancer; gene therapy; vector; 5T4 antibody; single chain antibody; mouse; human; 5T4Sabl
                                                       Conservative
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97GB-00013150.
97GB-00014230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 AA
                                                      Score 1275; DB 2;
Pred. No. 5.1e-64;
8; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ellard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5T4Sab1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carroll MW,
                                                                                Length 595;
-----GQSPTLLISYTSS
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers
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RESULT 57

AAO31101

ID AAO31

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                                                                               The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain variable and constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antibody; stem cell factor; mast cell
steel factor; c-kit ligand; gene therapy.
                                                                                                                                                                                                                                                                                                  New purified human antibody that binds to stem cell factor protein, useful for preparing a composition for treating asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Takeuchi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human A2-G8
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                                                                                                                                                                                                                                                  Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-523500/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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                                                                                                                                                                                                                                                  Page 47; 94pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                                                               ABR39844;
                              New antibodies comprising a heavy chain and a light chain complementarity determining regions from antibody 266, for treating and preventing conditions associated with the A beta peptide, e.g. Alzheimer's disease
                                                                                                                                                                                                                                           WO2003016466-A2
                                                                                                                                                                                                                                                                                                                              Hu266 N56T heavy chain.
                                                                                                                                                                                                                                                                                                                                                       18-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                      ABR39844 standard;
                                                                                  N-PSDB;
                                                                                                                                                                    17-AUG-2001; 2001US-0313224P
                                                                                                                                                                                           14-AUG-2002; 2002WO-US021322
                                                                                                                                                                                                                                                                                                    Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                            immunostimulant.
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                                                                                 2003-278557/27.
DB; ACC47228.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - VWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA----ISGSGGSTYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
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                                                                                                                    Vasquez
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Best Local Similarity
Matches 281; Conserv
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                                                                                                                                                                     LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
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 NHYTOKSLSLSPG
                                 NHYTOKSLSESPG 431
                                                                                            PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                               LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YC-----ASGD---YWGOGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
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                                                                       PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                                                                                                    SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.8%; Score 1274.5; ilarity 57.0%; Pred. No. 4.2a Conservative 30; Mismatches
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RESULT 59
ABR39848
ID ABR39
ABR39848;
                  ABR39848 standard;
                 protein;
                  461
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Hu266 N56T heavy chain

L8-AUG-2003

(first

Amyloid-beta; mmunostimulant. Abeta; antibody 266; nootropic; neuroprotective;

Homo sapiens

Disclosure; Fig 3;

82pp; English

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Best Local
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PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
               PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                              LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                    LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                                                                SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                     SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                  CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMI
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                                                                                                                                                                                                                                                                                                 -----KTLSVS-----TWT
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                                                                                                                                                                                                                                                                                                                                                                                                    GKGLELVAQINSVGTSTYYPDTVKGRFTIS-RDNAKNTLYLQMN-----SLRAEDTAVY
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57.0%; Pro
ative 30;
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Pred. No. 4.2e-64;
30; Mismatches 87
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Matches
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Hillman ,
                                                                                                                                                                                                                                                                                                       adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
                                                                                                                                                                                                                                                                                                                                           The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPs). These can used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                       New human immune system associated proteins (HISAP) encoding the HISAP, useful for diagnosing, treating or cell proliferative disorders or infections.
                                                                                                                                                                                                                                                                 Sequence 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune
                                                                                                                                                                                                                                                                                           erythematosus, arteriosclerosis, cirrhosis and cancer
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N-PSDB; AAC66522.
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                                                                                                                                  KILGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQ 114
                                                                                                                                                                                      RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQI
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KDYFPEPVTVSWNSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NH
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                              ----KTLSVS----
                                                      ------VGLRGGNYGMDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV 172
                                                                               KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473
                           ----QLELQDSG-----
                                                                                                                                                                                                             Score 1274.5; DB 4;
Pred. No. 4.3e-64;
9; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein HISAP-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating
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                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                       Length 473;
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The present invention relates to domain deleted CC49 or C2BB antibodies. Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2BB antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2BB construct where the CH2 domain has been deleted. Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from Hodgkin's lymphoma. Antibodies of the invention are also used to treat neoplastic disorder such as haematologic neoplasm, preferably non-Hodgkin's lymphoma. Antibodies of the invention are also used to treat neoplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tumour size, inhibiting tumour growth and/or prolonging the survival time of tumour-bearing animals and for treating
                                                                                                                                                                                                                                                      Novel domain deleted CC49 antibody reactive with tumor associated -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; CC49 antibody; C2B8 antibody; tumour associated antigen; neoplasm; neoplastic disorder; haematologic neoplasm; colon canon-Hodgkin's lymphoma; haematologic malignancy; tumour.
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16-NOV-2001; 2001US-0331481P
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                                                                                                                                                                                                                                                                                                                        C5E10; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial; neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulc dermatological; immunosuppressive; antiinflammatory.
29-JAN-2001; 2001US-0264318P
16-NOV-2001; 2001US-0331481P
21-DEC-2001; 2001US-0341858P
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Pred. No. 4.5e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a dimeric antibody (I) comprising several CC monomeric subunits, where the monomeric subunits are non-covalently cassociated. (I) is useful for treating a disorder especially immune CC associated. (I) is useful for treating a disorder, especially immune CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease, CC resistant Hodgkin's disease high grade, low grade and intermediate grade CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL), follicular CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma, CC lymphodenopathy, small lymphocytic B cell lymphoma, angioimmunoblastic CC lymphodenopathy, small lymphocytic, follicular, diffuse large cell. (CC lymphodenopathy, small lymphocytic, follicular, diffuse large cell.)

CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma, CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a CC detailed description of the various uses of (I)). The present sequence CC represents the antibody C5E10 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel dimeric antibody useful for treating immune disorder and neoplastic disorder, has several non-covalently associated monomeric subunits.
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 SPG
                                   SPG 431
                                                                                        NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                           SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
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                                                                                                                                                                                                                                                                                         NTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                               EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                                                                FPEPVTVSWNSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
                                                                                                                                                                                                                                                                                                                                                                                                  --KTLSVS-----QLELQDSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIK--NLKIEDSDTYICEVEDQKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLVLQLALLPAATQGNKVVLGKKG------DTVELTCTASQKKSIQF--HWKNSNQIK
                                                                     NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                    -ARCYYGSSPYFD---YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LALLFCLVTFPSCIL-SQVQLKESGPGLVAPSQSLSITCTVSGFSLTDYGVNWVRQPPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; 78pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1274; DB 6;
Pred. No. 4.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Matches 275;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a compound comprising CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions. The compound composition for the treatment of cancer, solid tumours, and as an adjuvant to surgical intervention to treat minimal residual disease. The present sequence is humanised murine antibody BIWA4 heavy chain protein
                                                                                                                                                                                                                                                                                                                                                                                Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compound useful for treatment antibody molecule conjugated to a under intracellular conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 15-16; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-2003
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                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            the invention
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                                                                                                       TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                                        QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------
                                                                                                                                                                                                                  S-RDNAKNSLYLQMN-----SLRAEDTAVYYCARQ------GLD------YWG
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                  EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                     THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                  ---QLELQDSG-----
                                                                                                                                                              RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                        LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70
                                                                                                                                                                                                                                                                                                  LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL-----TKGPSKL
                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody BIWA4 heavy chain protein.
                                                                                                                                                                                                                                                                                                                                        52.8%;
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                                                                                                                                                                                                                                                                                                                                        Score 1273.5; DB Pred. No. 4.5e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of cancer comprises CD44 specific highly cytotoxic drug, which cleaves
                                                                                                                                  TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                             69;
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                                                                                                                                                                                                                                                                                                                                                     Length 444;
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                                                                                                                                     Query Match
Best Local S
Matches 275
                                                                                                                                                                                                                     The present invention relates to novel antibody molecules comprising a variable region of the heavy (VH) and/or light chain (VL) of CD44v6 specific humanised antibody called BIWAB and BIWAA. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck, ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIWA4/8 antibody heavy chain mature protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                         New antibodies specific for an epitope coded by the variant exon of the CD44 gene, useful for treating cancer, including non-small cell lung, breast, head and neck, ovarian and lung cancer.
                                                                                                                                                                                            Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-2001; 2001EP-00112237.
26-SEP-2001; 2001US-0325147P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIWA8 antibody; heavy chain variable region; VH; VL; CD44v6; medicament; cancer; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIWA4/8 antibody heavy chain mature protein
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DB; AAD53212, AAD53215.
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                                                                                                                                                                                                                                                                                                                                                               24; Col 44; 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOEHRINGER INGELHEIM INT GMBH
BOEHRINGER INGELHEIM PHARM IN
                                                                                                                                                     Similarity
QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS--
                           S-RDNAKNSLYLQMN-----SLRAEDTAVYYCARQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                    NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                               LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI
                                                                                                           LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ostermann E, Pa
JJ, Van Dongen
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                                                                                                                                                 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patzelt
                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444
                                                                                                                                     Score 1273.5; DB 6;
Pred. No. 4.5e-64;
7; Mismatches 69;
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                                                                                                                                      Indels
                                                                                                                                                                 Length 444;
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                           GLD----YWG
                                                                                                                                     93;
                                                                                                                                     Gaps
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RESULT 65
AAR93553
ID AAR93
XX AAR93
XX AAR93
XX PAR93
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                                                                                                                                                                                                                        Claim 4; Page 16-18; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                     Human monoclonal antibody binds to cytomegalovirus 65 kD antigen produced by primer amplification, used in the diagnosis of hCMV
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-154852/16.
N-PSDB; AAT18059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody DNA heavy chain against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR93553 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP08038178-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; primer; amplify; PCR; light chain; MAb; 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR93553;
                                                                                                                                                                                                                                                                              infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TANA/) TANAKA H.
(NISN ) NISSHINBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Mature heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 kD hCMV antigen.
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The sequences given in AAR93553-54 represent the heavy and light chains respectively of a monoclonal antibody against a 65 kD antigen of human cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified using the sequences given in AAT18040-58. The monoclonal antibody may be used in the diagnosis of hCMV

Sequence 475 AA

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AAW11641
ID AAW1
XX
AC AAW1
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XX Huma
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                                                                                                                                                                                                                                          Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus; fusion protein; F-protein; vaccine; immunotherapy; therapy; Epstein Barr virus; immortalisation; recombinant antibody.
                                                                                                                                                                                                                                                                                             Human anti-RSV monoclonal antibody RF-2 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                       AAW11641 standard;
                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--N
                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSLSPG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYYDL----LTGSFPSYWGQGTLVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGKGLEWIGTIYYSGSTYYNPSLKSRYTISVDASNNQFSLKLSSYTAADTAVYYCARTSP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KILGNO--GSFLTKGPSKLNDRADSRRSL-WDQGN--FPLIIKNLKIEDSDTYIC-EVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGDSISRSSYSWGCIRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
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                                                                                                                                                                                                                                                                                                                      (first
/note= "complementarity determining 87. .118
                                                                           /note=
                          /label= CDR2
                                                              /label=
                                                                                                   /label= CDR1
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                                                  /note= "framework
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                                                                                                                                           /label=
                                                                                                                                                                  /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                            431
                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.8%;
58.1%;
                                                                                                                                                               = Leader_peptide
                                                                                                                            "framework
                                                                                     "complementarity determining
                                                                FR2
                                                                                                                                           FR1
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                                                                                                                                                                                                                                                                                                                                                                        475
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human monoclonal antibody specific for protein - used for the prevention and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                  LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKIL---
                                                                             EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                  DSFYLF----YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                             VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
                                                                                                            FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
                                                                                                                                       --KTLSVS-----TWTCTVLQNQKKV
                                                                                                                                                                                          VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                                                                                                                                                   ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS
                                                                                                                                                                                                                                          ----GNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE 117
              VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                                                    LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL
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ilarity 57.1%;
Conservative 2
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/note= "complementarity determining region
135. 145
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/note= "human
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146. .475
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                                                                                                                                                                                                                                                                                                                               Score 1273.5; DB Pred. No. 4.9e-64;
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RESULT 6:
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Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (Ig) I segment fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a leucine zipper motif. The Ig I segment is not necessary for binding of
                                                                                                                                                                                                                                      New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domatreating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                                                                                                    Claim 14; Page 58-59; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA52129.
                                                                                                                                                                                                                                                                                                                                                                                                                                Kavanaugh WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1999;
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266. .49
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157. .22
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note= "The Ig I segment and acid box are deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Human IgGl Fc_region
/note= "Contains hinge region
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 497
68
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                                                                                                                                                                                                                                                                                                                                                                          --QGGKTLSVSQLELQDSGTWTC-----TVLQNQKKVEFKIDIVPCP---
                                                     PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                         PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                       ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO
                                                                                                                                           ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                               SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                   EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                       -----APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                       TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
                                                                                                                                                                                                                                                                                                                                                                                                             AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWSIIMDSVVPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.8%;
57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1273.5; DB Pred. No. 5.1e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                                                                                                                                                                                              -GSS-----PSVQCRSPRGKNI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                  311
                                                                                        431
                                                                                                                                                                                               376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                     496
                                                                                                                         436
                                                                                                                                                            371
                                                                                                                                                                                                                                                                     316
                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                       256
                                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
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Key
Peptide
                                                                     immunoglobulin; G1; oligomerization domain; Fc region; fi
inhibitor; dimer; antagonist; cytostatic; anti-diabetic;
ophthalmological; anti-proliferative.
                                                                                              FGF-R; fibroblast growth factor receptor; extracellular domain; immunoglobulin; G1; oligomerization domain; Fc region; fusion pr
                                                Homo sapiens
 Location/Qualifiers
1. .21
/label= FGF-R1_sign
FGF-R1_signal_peptide
                                                                                               fusion protein;
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Human 04-DEC-2000

FGF-RI

(first entry)

Extracellular domain-Ig Fc fusion protein

AAY97171 standard;

protein;

525

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AAY97171;

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                                                                                                                                                                                                                                                                                                       Novel fusion protein constructs comprise a fibroblast growth factor (FGF) CC receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin CC (Ig) I segment fused to a heterologous oligomerization domain that CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 cegion, or light chain of an immunoglobulin molecule, or a peptide with a CC leucine zipper motif. The Ig I segment is not necessary for binding of CC acidic FGF and basic FGF (BGF). The Ig I deletion further increases the CC affinity for aFGF and heparin, protects the core of the molecule from CC proteolysis, and abrogates the heparin requirement for aFGF binding. The CC proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at CC subnanomolar concentrations and were 20-fold more potent than the FGF-R monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The CC fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-CC mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung, CC rectal, testis and cervical tumours), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma, wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g.
                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                  Sequence 525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domatreating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
                                                                                                                                                                                                                                                                                               postangioplasty and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 54-55; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2000; 2000WO-US003166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kavanaugh WM, Ballinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200046380-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-514961/46.
                                123
                                                                121
                                                                                                                                                                                                  276;
                                                                                                 70
                                                                                                                                73
                                                                                                                                                                  15
                                                                                                                                                                                                                Similarity
                                FGLTANSDTHLLQGQSLTLTLESPP------GSS-----PSVQCRSPRGKNI
                                                                TWSIIMDSVVPS----
                                                                                                                                KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
                                                                                                                                                                QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL
                                                                                               TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT
                                                                                                                                                                                                 Conservative
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87. .139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22. .285
/label= FGF-R1_extracellular_domain
/note= "Ig I segment is deleted"
37. .44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Human_IgG1_Fc_region
/note= "Contains hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Ig_II_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label=
                                                                                                                                                                                                                                                                                               postatherectomy restenosis)
                                                                                                                                                                                                                52.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig_III_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linker
                                                                                                                                                                                                 30;
                                                                                                                                                                                                                Score 1273.5;
Pred. No. 5.4
                                                               ----DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region and domains CH2 and
                                                                                                                                                                                                                .4e-64
                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                               525,
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                                                                                                                                                                                               Gaps
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                                163
                                                               167
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WPI; 2000-514961/46 Kavanaugh WM,

Ballinger M;

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RESULT 69
AAY97170
ID AAY97
XX AAY97
XX AAY97
XX 04-DE
XX FGF-R
KW inmun
XX FGF-R
KW inmin
KW inhib
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XX Ophth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                                                                      08-FEB-1999;
                                                                                                                                                                                                           07-FEB-2000; 2000WO-US003166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY97170 standard; protein; 622
                                                                                                                                                                                                                                                              10-AUG-2000.
                                                                                                                                                                                                                                                                                                                 WO200046380-A2
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                                                                                                        (CHIR ) CHIRON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- QGGKTLSVSQLELQDSGTWTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                        CORP
                                                                                                                                                        99US-0119002P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              'label= Human_IgG1_Fc_r
'note= "Contains hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Ig_III_segment
note= "This is the IIIc variant version"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= FGF-R1_extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Contains trhombin cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acid_box_segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig_II_segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC (Ig) I segment fused to a heterologous oligomerization domain that CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 CC region, or light chain of an immunoglobulin molecule, or a peptide with a CC leucine zipper motif. The Ig I segment is not necessary for binding of CR4 acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the Affinity for aFGF and heparin, protects the core of the molecule from CR5 proteolysis, and abrogates the heparin requirement for aFGF binding. The CR5 mew fusion polypeptides are better FGF inhibitors than FGF-R monomer CC proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at CC monomer protein as competitors of bFGF binding to immobilized FGF-R. The CC mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung, crectal, testis and cervical tumours), neovascularization (e.g. diabetic cretinopathy, neovascular glaucoma, wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. branches).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domated treating FGF-, angiogenesis-, or FGF receptor-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 51-52; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA52127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor (FGF-R)
                                                                      558
                                                                                                                                                                                                                                                                                           378
 618
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                                                                                                        368
                                                                                                                                              498
                                                                                                                                                                              308
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                                  LSPG
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                                                                                       SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHWHYTQKSLS
                                                                                                                                                             VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                                                                                                              DIVP----CPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKFKDTLMISRTPEVTCV
 Dasi
                                                                                                                                                                                                                                     VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                                                                                                                                                                                                                                                       GLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                                                                                                                                                                                               DKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLESRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLTANSDTHLLQGQSLTLTLESPP-----GSS------PSVQCRSPRGKNI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKV---
                                                                      SNGQPENNY
                                                                                                                                          VSNKALPAP:
                                                                                                                                                                                                                  VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKINDRADSRRSLW------DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIKILGNQGSFLTKGP
                                                                                                                                                                                                                                                                                                                                                                                                 -QGGKTLSVSQLELQDSGTWTC------TVLQNQKK------VEFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                     GLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein constructs
 621
                                  431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tein constructs comprise a fibroblast growth factor (FGF) extracellular domain (ECD) lacking the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.8%;
57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1273.5; DB 3; Pred. No. 6.5e-64; 1; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
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RESULT 70

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Best Local Sim
Matches 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1999;
15-FEB-2000;
02-MAR-2000;
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes Helicobacter-related disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 6; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kingsman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2000; 2000WO-GB004317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                           represents an Ig-5T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200136486-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of an Ig-5T4 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB83838 standard; protein; 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-343805/36.
                                                                                                                                   Similarity
                                                                                                                                                                                592
RYAGVPORFIGSGYGTDFTFTISTLQAEDLAVYFCQQD-
                             R-RSLWDQ-----GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL
                                                                                       TOGNKYVLGKKGDTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADS
                                                                                                                     Conservative
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2000GB-00003527.
2000GB-00005071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                 52.7%;
                                                                                                                                                                                                           fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM.
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                                                                                                                                 Score 1273; DB 4;
Pred. No. 6.5e-64;
                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll MW,
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                                                                                                                                               Length
                                                         -----GQSPTLLISYTSS
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 -YNSPPTFG
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RESULT 71
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AC ADE64
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                        This invention relates to a new antibody library which comprises at 10 cells, each of which comprises at least one integrated retroviral vector expressing an antibody light or heavy chain. Antibodies are of increasing importance in human therapy, assay procedures and diagnosti
                                                                                                                                                                                                          New antibody library comprising cells comprising at least one integrated retroviral vector expressing an antibody light or heavy chain, useful in preparing a composition for diagnosing or treating disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2002; 2002US-036BB0BP
10-APR-2002; 2002US-0371299P
28-MAR-2003; 2003US-00371299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody library; retroviral vector; antibody light chain;
antibody heavy chain; human therapy; multiplicity of infection; MOI;
plasmid; GATEWAY vector; LL2HCF.
                                                                                                                                                                                                                                                                                                                       N-PSDB; ADE64205
                                                                                                                                                           Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LL2HCF protein related to a novel antibody library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2003; 2003WO-US009662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003083077-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GALA-) GALA DESIGN
                                                                                                                                                                                                                                                                                                                                             2003-804051/75.
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                                                                                                                                                                                                                                                                                                                                                                                                 RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                           57pp; English.
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generating
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                           diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening antibody libraries containing large numbers of antibodies. The antibody library of the invention addresses this need, with the additional advantage of strict control over multiplicity of infection (MOI), and is useful in preparing a composition for diagnosing or treating a wide variety of disorders. The present sequence is the amino acid sequence of the LL2HCF protein, which was encoded by the Gatteway retroviral vectors used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 465 AA;
                                392
                                                                  365
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425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 KKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                     QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
                                                                                                                                                                                                                                                                     VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDKTHTC
                                                                                                                                                                                                                                                                                                                                             VTVSSASTKGPSVFPLAPSSKSXSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GNFP-----LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
                YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                      AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                      PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                          ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                           LTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------QL 174
                                                                QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                                    AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                                                                                                                           ELQDSG-----
                                                                                                                                                                                                                                                                                                                                                                                                               ATITADESTNTAYMELSSLRSEDTAFYFCARRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPGSSVKVSCKASGYTFTSYWLHW-----VRQAPGQGLEWIGYINPRNDYTEYNQNFKDK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                           ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1272.5;
Pred. No. 5.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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les 76;
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464
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28-MAY-1999;
                                                07-DEC-2000
                                                                           Homo sapiens
Synthetic.
                                                                                                autoimmune
                                                                                                       Anti-Death
                                                                                                                    Chimeric 4H6 anti-DR4 antibody heavy chain protein.
                                                                                                                                   15-MAR-2001
                                                                                                                                                              AAB49243 standard;
                                 25-MAY-2000;
                                                              WO200073349-A1
       (GETH )
                                                                                                       receptor 4; DR4; antibody; apoptosis; cancer; arthritis;
                                  2000WO-US014599
                                                                                                                                  (first entry)
                     99US-00322875
                                                                                                                                                             protein; 476
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GENENTECH INC

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RESULT 73
AAY50151
ID AAY50
XX AAY50
XX AAY50
DT 17-OC
DT 31-JA
XX AAT1L
KW AMMER
KW Teact
KW Immur
KW OVART
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Best Local S
Matches 273
          humanisation; complementarity determining region; CDR; CDR grafting; reactive stroma; fibroblast; epithelial cancer; diagnosis; immune response; framework sequence; constant region; variable region; producibility; treatment; cancer; colorectal; lung; breast; head; neck; producibility; treatment; cancer; colorectal; lung; breast; head; neck; overian; lung; bladder; pancreatic; metastasis; dejection; wound healing; overian; lung; bladder; pancreatic; metastasis; dejection; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to an anti-Death receptor 4 (DR4) antibody. The antibodies of the invention are useful for inducing apoptosis in mammalian cancer cells such as colon cancer cells and for treating an immune-related disease in a mammal such as arthritis and autoimmune
                                                                                                                                                                17-OCT-2003
31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 476
                                                                                             Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
                                                                                                                                Antibody F19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-death receptor 4 antibodies useful for treating cancer e related disorders such as rheumatoid arthritis, sjogren's ome, Grave's disease and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                               etandard;
                                                                                                                                                                                                                                                                                                                                                  SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                      RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPSVQCRSPRGKNIQGG------KTLSVS------QLELQDSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVFLKMNSLQTDDTAMYYCAREGEFD-----YYGSSLLS-YHSMNFWGQGTSVTVSSAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAVGSTNYNSALMSRLSISKDNSKS
                                                                                                                                                                                                                                                                                                                               SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLIIK--NIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLTLESPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 18; 126pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                chimeric mouse/human heavy chain variable region (chF19HC)
                                                                                                                                                              (revised)
(first entry)
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                                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                               453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1272;
Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                               475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the heavy chain variable region of a chimeric compuse/human F19 antibody (chF19HC). F19 (ATCC Accession number HB 8269) compused human F19 antibody (chF19HC). F19 (ATCC Accession number HB 8269) computed the computed his a cell surface molecule of reactive stromal computed his a highly consistent molecular trait of the reactive stroma of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use computed his reproblematic as it elicits a human anti-mouse response which creduces the efficacy of the antibody in patients and impairs continued administration. This chimeric antibody was humanised by joining entire murine variable regions to human constant regions. However, humanised cantibodies produced by this method can still elicit an anti-mouse componse in humans, whereas antibodies humanised via CDR (complementarity determining region) grafting are less immunogenic in humans. Humanised componse in humans are useful for treating cancers e.g., colorectal cancers, conon-small cell lung cancers, breast cancers, head and neck cancers, continued content cancers, lung cancers, bladder cancers, head and neck cancers and content cancers. They are also useful for the detection of activated content patient. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park JE, v
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody protein, useful of activated stromal fibrobla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP953639-A1
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o sapiens.
                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                             271;
                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                               453
                                                                                                                                                                                                                               W---DQGNFPLIIKNIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
   PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                     ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP
                                                                                                  LQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-
                                                                                                                                TLESPPGSSPSVQCRSPRGKNIQGG-----
                                                                                                                                                                                               TVGKSSSTAYMELRSLTSEDSAVYFC-----ARRIAYGY---DEGHAMDYWGQGTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garin-Chesa
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143pp; English
                                                                                                                                                                                                                                                                                                                                              52.7%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , useful for treating cancer and fibroblasts in healing wound or
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                                                                                                                                                                                                                                                                                                                                              Score 1271.5; D
Pred. No. 6e-64;
                                                                                                                                                                                                                                                                                                                               Mismatches
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KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ

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                           The invention describes a binding domain-immunoglobulin fusion protein that is capable of at least one immunological activity, comprising a binding domain polypeptide fused to an immunoglobulin hinge region polypeptide capable of specifically binding to an antigen, or an immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
                                                                                                                                                                                                                                                             New human binding domain-immunoglobulin fusion protein useful for treating a subject having or suspected of having a B-cell disordemalignant condition e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse; neuroprotective; gene therap; single chain antibody; variable fragment; scFv; binding domain-immunoglobulin fusion protein; B-cell disorder; malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis; Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus; multiple sclerosis; systemic hugus erythematosus; Sjogrens syndrome; immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease; unlcerative colitis; inflammatory bowel disease; immunological effector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001US-00765208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2002; 2002WO-US001487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mediated cytotoxicity; complement dependent cytotoxicity; lement fixation; mouse; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JA,
                                                                                                                                                                                                    Page 120-121; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayden-Ledbetter
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266. .499
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fragment (scFv)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Human immunoglobulinG1
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                                                                                                                                                                                                                                                          e.g.
polypeptide
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   or to the
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CH3 domains"
                              polypeptide fused
                                                                                                                                                                                                                                                                                              disorder
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RESULT 75
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(first entry

ADD25587

standard;

protein; 499

Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; Binding domain-immunoglobulin fusion protein-associated protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                      426
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                                      LSLSPG
                                                                          WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                       WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                      CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                             CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
                                                                                                                                                                                                                                                                  CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
                                                                                                                                                                                                                                                                                                                              FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
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                                                                                                                                                               CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---
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Pastst
                                                                                                                                                                                                                                                                                                                                                                  IDI-----VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT
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neuroprotective; hinge region; immunoglobulin heavy CH2 constant region; CH3 constant region; IgG1;

chain

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CC comprising a binding domain polypeptide, an immunoglobulin heavy chain CC (H2 constant region polypeptide, and immunoglobulin heavy chain CC (H2 constant region polypeptide, and an immunoglobulin heavy chain CC polypeptide, and an immunoglobulin heavy chain CH2 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and the CH2 constant region polypeptide. The first cysteine region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine residues, where the first cysteine is not mutated, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine is not mutated, a cysteine residue, and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more than one (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more than one (cysteine residues, and a mutated human IgG1 immunoglobulin hinge region polypeptide contains to more than one (cysteine residues. The binding domain polypeptide contains to more than one (cysteine residues. The binding domain insulpedial activity comprising antibody capable of at least one immunoglobulin hinge region polypeptide contains (constitue the cell mediated cytotoxicity (ADCC) and complement fixation. The binding domain immunoglobulin fusion protein is constitue, producing the polymucleotide and a carrier, and complement fixation. The binding domain immunoglobulin fusion protein, a producing the binding domain. Immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain. Immunoglobulin fusion protein, a pharmaceutical romain immunoglobulin fusion protein, a pharmaceutical romain immunoglobulin fusion protein, a malignant condition or a B-cell disorder. Fig. 1 disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, multiple collected at a sarrier. The sequence is a bindin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
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Sequence 499

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Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding domain; immunoglobulin; fusion protein; cytostatic; antiathritic; immunosuppressive; antidiabetic; antithyroid neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1;
                          17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD25454 standard; protein; 499
                                                                                                                                                                                                                                                          US2003118592-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding domain-immunoglobulin fusion protein-associated protein
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                                                                                                                                                                                                                                                                                                                                                                     type I diabetes
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                                                                                                                                                                                                                                                                                                                                                                     condition; B-cell disorder; melanoma; carcinoma; sarco
d arthritis; myasthenia gravis; Grave's disease;
abetes mellitus; multiple sclerosis; autoimmune disease
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Pred. No. 6.76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antithyroid;
eavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                             carcinoma; sarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC computating a binding domain polypeptide that is fused to an CC computating domain polypeptide, an immunoglobulin heavy chain CC constant region polypeptide that is fused to the hinge region CC polypeptide, and an immunoglobulin heavy chain CH2 constant region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide that is fused to the CH2 constant region polypeptide. The CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide; derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a cc mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine region polypeptide, derived from CC immunoglobulin hinge region polypeptide, derived from CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from CC cysteine residue; The binding domain-immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunoglobulin hinge region polypeptide contains no cysteine residued are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising to binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising to binding domain-immunoglobulin composition comprising to bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           Matches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence brullpocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                        SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI
                                                                                                                 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR----
                                                                                                                                                                      RFSGSGSGTSYSITISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG
                                                                                                                                                                                                                               RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL--------
                                                                                                                                                                                                                                                                                       SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA
                                                                                                                                                                                                                                                                                                                                                TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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     --GKNIQGGKTLSV----
                                                                                                                                                                                                                                                                                                                                                                                                     52.7%; Score 1271.5; DB 7; 56.6%; Pred. No. 6.7e-64; tive 27; Mismatches 93;
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----SQLELQDSGTWTCTVLQNQKKVEFK 196
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                                                                                                                 ---SPR----
                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ABP58275
ID ABP58
XX ABP58
XX ABP58
XX 23-OC
DT 31-M2
XX MONOC
DT 31-M2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                        30-APR-2001; 2001US-0287539P
                                                                                                                                                                                                              26-APR-2002; 2002WO-US011853
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised 3D6
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31-MAR-2003
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                                   2003-183835/18.
DB; ABZ24633, ABZ24635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody heavy chain.
                                                                                             Vasquez M;
                                                                                                                                                                                                                                                                                                                                                118
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                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
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/note= "the mature heavy chain is claimed in Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= Signal_peptide
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54
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                                                                                                                                                                                                                                                                                                                                                                                                        "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                            "heavy chain variable region, claimed in Claim 4"
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New humanized forms of mouse 3D6 antibodies, useful for treating Down's

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RESULT 78
AAR93166
ID AAR9
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AC AAR9
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AC AAR9
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AC AAR9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a preferred heavy chain of a humanised CC antibody of the present invention. In the variable region of this CC sequence, the complementarity determining regions (CDRs) originate from CC murine monoclonal antibody 3D6 and the framework region from human CC germline VH segment DP-45 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These cC humanised antibodies shave binding affinities (affinity and epitope CC location) approximately the same as those of the mouse 3D6 antibody. The CC invention includes antibodies, single chain antibodies, and their CC fragments, as well as nucleotide sequences, vectors, transformed host CC cells, and methods of using the humanised antibody to treat, prevent, CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plaque in the brain.
   30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 468
                                    AAR93166;
                                                                     AAR93166
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                                                                                                                                                          450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       TQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
                                                                      standard;
                                                                                                                                                                                     HEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                   VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                                     LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
                                                                                                                                                                                                                                                                                                                                                                                               DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQGG-----CTLSVS-----QLELQDSG-----
                                                                                                                                                                                                                               VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
                                                                                                                                                                                                                                                                                                                                                                      DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKKSIQFHWKNSNQIKILGNQGSFL--TKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNFGLSLIFLVLVLKGVQCEVQLVESGGGLV---QPGGSLRLSCAGSGFTFSNYGMSWVR
                                                                                                                                                          HEALHNHYTQKSLSLSPG
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   (first entry)
                                                                     protein;
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                                                                      472
                                                                                                                                                          467
                                                                                                                                                                                             431
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Pred. No. 6.6e-64;
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                                                                      ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Best Local Sin
Matches 270;
                                                                                                                                                                                                                                                                                                               The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal
                                                                                                                                                                                                                                                                         Sequence 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monoclonal rhesus positive; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant anti-rhesus I transformed insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        babies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR2724182-A1
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LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAP
                                                                                                                                      WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
                                                      STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
                                                                                                           TSKNQFSLKLNSVTAADTAVYYCARAPE-----YKWKYHGDWFDPWGQGTTVTVSSA 143
                                                                                                                                                                 KPSETLSLTCTVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVD
                                                                                                                                                                                         KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQ--GSFLTKGPSKLNDRADSRRSL---
                                                                                 PGSSPSVQCRSPRGKNIQGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 35-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margaritte
                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= heavy_chain
/note= "human gamma 1 chain constant region
variable region from anti-rhesus D antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= signal_peptide
/note= "mouse VH signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rhesus negative; haemolysis; gamma 1 heavy chain; insect host cell; baculovirus; recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; immunoglobulin isotype
                                                                                                                                                                                                                     52.7%; Score 1271; DB 2; 59.5%; Pred. No. 6.7e-64; tive 25; Mismatches 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody - expressed by baculovirus-
and useful for preventing haemolysis in new-born
                           -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                           French
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                     2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSplA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease. (Updated on 17-OC7-2003 to standardise OS field)
                                                                                                                                                                                                          Monkey monoclonal antibody binding | for treating auto:immune disease or
                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; he
                                                                                                                                                                                   Claim 14;
                                                                                                                                                                                                                                                                                       Anderson DR, Brams
                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca; cynomolgus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primatised anti-human B7.1 antigen antibody 16C10 heavy
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25-MAY-1997
                                                                                                                                                                                                                                                                                                                  (IDEC-) IDEC
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DB; AAT62513.
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                                                                                                                                                                                   Fig 10B; 81pp;
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(first en
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disease.
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Sequence 476 AA;

New monoclonal antibodies specific for inhibiting binding to CD28 - useful as

: B7.1 or B specific

B7.2 antigens and

immunosuppressants

for

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RESULT 80
AAW63765
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Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                          Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; T cell/B cell interaction; tumour; inflammation; imaging agent; vac immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobuli
                                  N-PSDB;
                                                                                                                                                                                                                        Macaca fascicularis.
                                                                                                                                                                                                                                                                                                                                                29-SEP-1998
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                                               WPI; 1998-286601/25.
                                                                                                                       08-NOV-1996;
                                                                                                                                               29-OCT-1997;
                                                                                                                                                                       14-MAY-1998
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                                                                                                                                                                                                                                               proliferation.
                                  AAV35489
                                                                                                                                                                                                                                                                                                                        primatized 16C10 heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISTOTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY----NNWFDVWGPGVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
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                                                                                                PHARM CORP
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                                                                        Hanna
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                                                                                                                                                                                                                                                                                                                        protein.
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                                                                                                                                                                                                                                                           imaging agent; vaccine;
IgG; immunoglobulin G;
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RESULT 81
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AC AAU1
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Best Local (
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                     Protein sequence
                                                         12-MAR-2002
                                                                                                                               AAU11646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                           KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                     YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                         TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 AA;
                                                                                                                                                                                                                                                                                               YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISTOTSKNOFSLKLNSMTAADTAVYYC-VRORLFSVVGMVY-----NNWFDVWGPGVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
                                                                                                                                                                                                                          KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                         (first entry)
                   of primatised
                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Mismatches
                                                                                                                                 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1271; DB 2;
Pred. No. 6.8e-64;
                     form
                     of.
                     the
                     heavy
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                                                                                                                                                                                                                          475
                                                                                                                                                                                                                                                             431
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                     chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 68;
                     of 16C10 antibody
                                                                                                                                                                                                                                                                                                   437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Macaca sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; macaque monkey; light chain; primatised antibody; 16C10 antibod neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD86; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; tumour; b cell lymphoma; B cell leukaemia; autoimmune disease; immunosuppression; organ rejection; interleuking; antigen; organ rejection; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of monoclonal antibody which specifically binds to B7.1 antigen CD and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 5b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2001; 2001WO-US016364.
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                                                                             144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                                                                          VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                ODSG-----
                                                                                                                                        LESPPGSSPSVQCRSPRGKNIQGG------KTLSVS---
                                                                                                                                                                                                                                                                                                                              LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
                                                                                                                                                                                                                                                                                                                                                                                     LGKKGDTVELTCTASO---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS
                                                                                                                                                                                                  ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ß,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1271; DB 5;
Pred. No. 6.8e-64;
9; Mismatches 87
            -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
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                                                                                                                                        -- QLEL
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                   216
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QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP

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RESULT 82
ADD25787
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         The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the cH2 constant region polypeptide. The hinge region polypeptide to the CH2 constant region polypeptide. The hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge contains 2 cysteine residues, where the first cysteine is not mutated; a
                                                                                                                                                                                                                                                                            New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; 1gG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-801317/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUL-2002; 2002US-00207655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding domain-immunoglobulin fusion protein-associated protein #160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD25787 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENECRAFT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                         SEQ ID NO 348; 157pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                             Hayden-Ledbetter MS,
immunoglobulin hinge region polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                             Thompson
derived
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CC immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region CC polypeptide, derived from (a) having 3 or more cysteine residues; where CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains CC no cysteine residues. The binding domain immunoglobulin fusion protein is CC capable of at least one immunological activity comprising antibody CC dependent cell-mediated cytotoxicity (ADCC) and comprising antibody CC dinding domain polypeptide is capable of specifically binding to an CC enstruct comprising the polynucleotide encoding the Dinding domain-immunoglobulin fusion protein, a recombinant expression CC construct comprising the polynucleotide (operably linked to a promoter), CC a host cell transformed or transfected with a recombinant expression CC construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin cCC fusion protein or polynucleotide and a carrier, and treating a subject CC having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain fusion protein sequence multiple successory sequence, the protein sequence is a binding domain fusion protein sequence is a binding domain fusion protein-associated protein sequence. Note: The creation and is also available in electronic formed part of the printed specification can be entired to the printed specification can be entired to the printed specification can be entired by sequence and is also available in electronic formation fusion protein sequence. Note: The content sequence not sequence is a binding domain can be entired by sequence and content sequence is a binding domain fusion protein entired part of the 
                                                                  seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (a) having 3 or more cysteine residues, where the mutated human
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Matches 282; Query Match Local Similarity Conservative 52.7%; 29; Score 1271; DB 7; Pred. No. 7.2e-64; Mismatches 92; Length Indels 110; Gaps 13;

밁 Ś Ś 밁 밁 Ś 밁 8 밁 Ś 5 문 5 맑 밁 411 339 351 279 291 231 174 171 219 154 117 66 TVKLL----IYYT---SRLHSGVPSRFSGSGSGTDYSLTIANLQPEDIATYFCQ-----58 QIKILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKE 116 19 1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW----KNSN 57 LLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTVSSDQEPKSCDKTHTCPPCPAPE ---LELQDSGTWTCTVLQNQKKVEFKID-----IVPCPAPEPKSCDKTHTC----PE SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EVQLLVFGLTANSDTHLLQGQSL-------TLTLESP----PGSSPSV 153 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431 SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE KASGYSFTGYIVNWLKQSHGKNLEWIGLINPYKGLTTYNQKFKGKATLTVDKSSSTAYME -- QGNTLPWTFGGGTKLVTKRELGGGGSGGGGSGGGGSIDEVQLQQSGPELVKPGASMSC -----RSPRGKNIQ-------MTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDG -GGKTLSVSQ-----398 230 170 410 350 290 173 65

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ABP58289
XX ABP5
XX Mono
XX Regi
FT Re
                                                                          The present sequence is the protein sequence of the heavy chain of a Chumanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine complementarity determining regions (CDRs) originate from murine complementarity determining regions (CDRs) originates from human garmine VH segment DP-28 and the framework region originates from human garmine VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These chumanised antibodies have binding affinities (affinity and epitope continuous antibodies have binding affinities (affinity and epitope continuous includes antibodies, single chain antibodies, and their fragmente, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, as leviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or cherwise ameliorate symptoms and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; 10D5; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 13-15; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinton PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001; 2001US-0287653P
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31-MAR-2003
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Sequence 472

New human type complementation-determining region-transplanted and derivatives against ganglioside GD3, useful in diagnosis are of e.g. tumors, with low antigenicity, little side effects but

ed antibody and therapy

therapy

Claim 41; Page 168-172; 183pp; Japanese

activity

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RESULT 84
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Best Local Sin
Matches 279;
                                                                                                                                                                                                                        Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ganglioside GD3 specific antibody related protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB81987;
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                                                                                                                                                                          WPI; 2001-266143/27.
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                                                                                                                                                                                                                     Shitara K,
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Pred. No. 7.26
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RESULT 85
AAU87089
ID AAU87
XX AAU87
XX AAU87
XX AU87
AC AAU87
XX D5-JU
XX Sigle
XX Humar
KW Limmur
KW Limmur
KW Limmur
KW Limmur
KW Synth
XX Homo
OS Synth
XX WO200
XX 31-JA
PF 20-JU
XX E1-JU
XX (BRIP
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$36668
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Best Local S
Matches 271
                                                                                                                                                                                                             immune
tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification
                             21-JUL-2000; 2000US-0220139P
                                                                                                                      WO200208257-A2
                                                                                                                                                                                                                                                                     Siglec-BMS-L3a-hIg fusion protein (Siglec-BMS-L3a-hIg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 582 AA;
                                                         20-JUL-2001; 2001WO-US023082
                                                                                                                                                                                                                                                                                                                                                               AAU87089 standard;
                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271;
                                                                                                                                                                                          sialic acid-binding Ig-related lectin; SIGLEC; asthma; system disease; leukaemia; allergy; inflammatory disease; damage; allergic rhinitis; osteoarthritis; Crohn's disease; sis; rheumatoid arthritis; conjunctivitis.
BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNQGSFLT---KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-----LOLDETCAEAQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTYYSDSVKGRFTIS-RDNSKNTLY-----LQMRSLRAEDSAVYFC-----TRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                       GKAPTSSSTKKTQLQLEHLLLDLQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTLSVS-----TWTCTVLQNQKKVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGTYYFDS-----WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                  entry
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Pred. No. 9
8
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Sequence

619

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CC are useful for treating immune system diseases such as asthma, leukaemia accor other altergic or inflammatory diseases. Extracellular domains of (I) crepresent potential markers for screening, diagnosis, prognosis, follow-cc up assays, and imaging methods. (I) is useful as a target for drugs which inflammatory diseases such as allergic rhinitis, osteoarthritis, crimination, tissue damage and remodeling in asthma, and circular inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's cdisease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (I) is cdisease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (I) is clientifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence cuseful in diagnosis and/or prognosis methods, and to detect the presence cond/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS condicible are useful as nucleic clone of SIGLEC-BMS gene copy number is determined for detecting cdiseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

ANUBTO74-AAUBTO89 represent human SIGLEC amino acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protei molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's dise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated SIGLEC (sialic acid-binding related lectin) protein (I). Pharmaceutical compositions comprisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Longphre M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compositions comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease.
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Ş 8 S 밁 á á 밁 5 밁 밁 밁 밁 Ş Query Match Best Local S Matches 273 447 387 331 260 205 273; 181 œ Similarity NQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQ-----PEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK -----VLONRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALD PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 319 PRGKNIQGGKTLSVSQ------LELQDSGTWTCTVLQ--NQKKVEFKIDIVPCPA -----KEEVQLLVF-----GLTANSDTHLLQGQSLTL---TLESPPGSSPSVQCRS RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSW------RHLLLVLQLALLPA---ATQGNKVVL-GKKGDTVELTCTASQKKSIQFHWKNSNQIKILG FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK -RISWTORGOVISPSOPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV---HD LSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPA------Conservative 52.6%; 27; Score 1270; DB 5; Pred. No. 1e-63; Mismatches 90; Length 619; Indels Gaps 379 446 330 114 53

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RESULT 86
ABB99224
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                                                                                          Query Match
Best Local S
Matches 275
                                                                                                                                                                   The invention relates to a novel binding molecule comprising at least one antigen binding site comprising in sequence the hypervariable regions CDR1, CDR2 and CDR3. The molecule of the invention has immunosuppressive, antipsoriatic, antiinflammatory, and antiallergic activity. The molecule of the invention is a CD45-Antagonist. The binding molecule or humanised antibody is useful as a pharmaceutical in the treatment of autoimmune diseases, transplant rejection, psoriasis, inflammatory bowel disease and allergies. The binding molecule has a binding specificity for both CD45RO and CD45RB in medicine, where the binding molecule is a chimeric, a humanised or a fully human monoclonal antibody. The sequence represents the heavy chain of the CD45RO/RB binding molecule
                                                                                                                                                                                                                                                                                                                                                             New binding molecule having at least one antigen binding site, useful a pharmaceutical in the treatment of autoimmune diseases, transplant rejection, psoriasis, inflammatory bowel disease and allergies.
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
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                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD45-Antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive;
               80
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                                                                                            l Similarity
275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVARTIS AG.
NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                 448
                                                                                                                                                                                                                                                                                                                                                                                                                                              JW,
ADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                                                                                                    Page 31; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD45RO/RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein; 448
                                     LVKPGASVKMSCKASGYTFTNYIIHWVKQEPGQGLEWIGYFNPYNHG-----TKYNEK
                                                              LGKKGDTVELTCTASQKKSIQF---HW----KNSNQIKILG-----NQGSFLTKGPSKLNDR
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kolbinger
W, Hall BM
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD45RO; CD45RB; binding
                                                                                                                                                 ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR2
99. .107
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
50. .66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5RO; CD45RB; binding molecule; CDR1; CDR2; CDR3;e; antipsoriatic; antiinflammatory; antiallergic;autoimmune disease; transplant rejection; psoriasis;el disease; allergy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                         BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding molecule heavy chain.
                                                                                                       52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carballido Herrera
                                                                                         Score 1269.5; DB 5
Pred. No. 7.7e-64;
7; Mismatches 73;
                                                                                                                  DB 5;
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                                                                                            Indels
                                                                                                                    Length
                                                                                                                     448;
                                                                                          , 68
                                                                                          Gaps
                                       63
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AAY94408
ID AAY94
XX AAY94
XX AAY94
XX AAY94
XX 11-SE
XX Human
XX Human
KW Human
KW Human
KW Human
KW Human
KW O2-DE
XX O2-DE
XX 02-DE
XX 02-DE
XX WPI;
DR N-PSI
XX WPI;
DR N-PSI
XX WPI;
DR N-PSI
XX WPI;
CC Gegener
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            The present sequence is a fusion protein comprising part of human VCAM-1 and the FC region of human IgGI. The sequence encoding this protein was generated by integrating the VCAM-1 coding region into a plasmid designated pDEF24/IgGI, which encodes the hinge and constant CH2-CH3 domains of human IgGI. The sequence was then ligated to the expression vector pDEF24 and transformed into DH5a competent cells. The fusion protein was used as a control in adhesion experiments involving
                                                                                                                                                                                    Nucleic acids encoding ACAM, a human cellular adhesion molecule, for diagnosing, preventing and treating diseases associated with expression and activity, e.g. epilepsy and schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant; dementia; epilepsy; schizophrenia; peripheral nerve injury; diabetic neuropathy; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human VCAM-1/IgGI-Fc fusion protein.
                                                                                                                                                     Example
                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                               Hoekstra
                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                 (ICOS-) ICOS
                                                                                                                                                                                                                                                           2000-422952/36.
DB; AAA30442.
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length variants of a novel adhesion molecule designated ACMA. ACAM.

nucleic acids and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate ACAM expression and activity such as dementia, epilepsy, schizophrenia, peripheral nerve injuries and diabetic neuropathies. They may be used to rectify mutations or deletions in a patient's genome that affect the activity of ACAM or to supplement insufficient ACAM production in a patient. Conversely, antisense nucleic acid molecules may be administered to down-regulate ACAM expression. The nuclectide sequence may also be used as a DNA probe in diagnostic assays (e.g. PCR) to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence determine which patients may be in need of restorative therapy. ACAM polypeptides may be used as antigens in the production of antibodies against ACAM and in assays to identify modulators (agonists and antagonists) of ACAM
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Best Local Similarity 59.1
Matches 264; Conservative
                                                                                                Synthetic.
                                                                                                                                                                                                                                                 CD19:zeta chimeric immunoreceptor.
                                                                                                                                                          antiarthritic;
                                                                                                                                                                                       CD19; chimeric;
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                                                             Homo sapiens.
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Location/Qualifiers
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59.1%; Pred. No. 1.3e-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to genetically engineered CD19-specific immune CC cells which express, and bear on the cell surface membrane, a CD19-cC specific chimeric receptor. The CD19-specific chimeric T cell receptor CC consists of: (a) an intracellular signaling domain selected from zeta, ceta, delta, gamma or epsilon chain pf CD3, MB1 chain, B29, FcgammaRIII CC and FcepsilonRI, for an effector function of the immune cell; (b) at cleast 1 transmembrane domain and (c) at least 1 extracellular domain CC comprising a CD19-specific receptor. The compositions and methods of the present invention are useful for cellular immunocherapy of CD19 CC malignancies and for abrogating any untoward B cell function in CC autoimmune disorders such as lupus or rheumatoid arthritis. The present sequence represents a CD19:zeta chimeric immunoreceptor amino acid cequence. This chimeric receptor was constructed by PCR splice overlap CC extension and consists of human GM-CSF receptor alpha chain leader cpeptide, FMC63 Vh, Gly-Ser linker, FMC63 Vl, human IgG1 FC, human CD4 transmembrane domain and human cytoplasmic zeta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 287; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetically engineered CD19-specific immune cells, useful for cellular immunotherapy of CD19 malignancies and for abrogating any untoward B continuation in autoimmune disorders such as lupus or rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                    62 PDGTVKLLIYHTSRLHSGVPSRFSGSGSGT-----DYSLTISNLEQEDIATYFCQQGN 114
                                                                                                                                                                                                                                                                                                                                                                                           55 NSNQIKILGNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVED 113
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                                                                 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                           LQDSGTWTCTVLQNQKKV----BFKIDI-----VPCPAPEPKSCDKTHTC-----PELL
                                                                                                                                                                                                                                                                                                                            QKE-----SVQLLVFGLTANSDTHLLQGQSLT----LTLESPPG-----SSPSVQC---- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLVLQLAL--LP-----AATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---K
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                    TLPYTFGGGTKLEITGSTSGSGKP-GSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSG 173
                                        GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                      TDDTAIYYCA----KHYYYGGSYAMDYWGQGTSVTVSSVEPKSSDKTHTCPPCPAPELL
                                                                                                                                                                                                    VSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                            -RSPRGKNIQ-----GGKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 1268; DB 6; 56.2%; Pred. No. 1.3e-63; ive 28; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raubitschek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 102;
                                                                                                                                                                                                                                            ----LSVSQLE 175
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RESULT 89
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                                                                                                                                                                    Query Match
Best Local Sim
Matches 274;
                                                                                                                                                                                                                                                                                                                                The invention relates to treating cognitive symptoms or reducing disease progression in a subject having a condition or disease associated with amyloid-beta peptide (Abeta). The method involves administering an amount of an anti-Abeta antibody that has greater affinity for soluble Abeta than 10^-9 M, that has affinity (KD) for soluble Abeta-40 or Abeta-41 higher than 10^-9 M, or that has greater affinity for soluble Abeta than antibody 266 has. The method or the anti-Abeta antibody is useful in preparing a medicament for treating cognitive symptoms or reducing disease progression in a subject having a condition or disease associated with Abeta. The condition or disease is Alzheimer's disease, Down's syndrome, cerebral amyloid angiopathy, vascular dementia, or mild cognitive impairment. The present sequence represents a humanised anti-Abeta antibody 266 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or reducing the progression of diseases associated with an beta peptide, e.g. Alzheimer's disease, vascular dementia or mild cognitive impairment, comprises administering an anti-amyloid-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-2001; 2001US-0313576P.
28-MAY-2002; 2002US-0383851P.
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 20-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2002; 2002WO-US021324.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-Abeta
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  NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                       LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI
                                                                                                               LGKKGDTVELTCTAS -- QKKSIQFHWKNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody 266 heavy chain.
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                                                                                                                                                                 Score 1267.5; DB 6;
Pred. No. 9.9e-64;
26; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised 266 antibody heavy
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Mus sp. Synthetic. 17-AUG-2001; 2001US-0313222P 28-MAY-2002; 2002US-0383846P 14-AUG-2002; 2002WO-US021323 27-FEB-2003 WO2003015691-A2

mutein.

(ELIL) LILLY & CO ELI.

Bales ģ Dodart JF,

2003-268234/26.

Effecting rapid improvement of cognition in a subject having disease, Down's syndrome, cerebral amyloid angiopathy, or mil impairment, comprises administering anti-A beta antibody. having Alzheimer' or mild cognitiv

Disclosure; Page 21-23; 85pp; English.

The present invention relates to a method for effecting rapid in of cognition in a subject having a condition or disease related Abeta peptide. The method comprises administering an anti-Abeta The method is useful for treating cognitive impairments associate. peptide including those involved in Alzheimer's di associated with improvement antibody ç

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  17-AUG-2001; 2001US-0313221P
17-AUG-2001; 2001US-0313224P
23-OCT-2001; 2001US-0334987P
                                                                                                                                                                                                                                                                                                                                                        Complementarity determining region; CDR; humanised; mouse; heavy; variable; domain; antibody; preclinical; clinical; Alzheimer's disease; epitope; amyloid beta peptide; Abeta; central nervous system; plasma.
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05-NOV-2002

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standard;

protein;

Immunoglobulin; Anti-tissue factor

promoter; cytostatic; antiinflammatory;

immunomodulator;

(TF) heavy chain fragment.

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                                                                                                                                                                    SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                  SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                      EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                        THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                            TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                                                                                      PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                       --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                               QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-RDNAKNTLYLOMN-----SLRAEDTAVYYC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGKKGDTVELTCTAS--QKKSIQFHWKNS-----NQIKILGNQGSF--LTKGPSKL
                                                                                                                                                                                                                        PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                          THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1267.5; DB Pred. No. 9.9e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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binds an e
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                                                                                                                                                                                                                                                                                                                                                               (1g), comprising a first or second promoter-cistron pair consisting of a first or second promoter and cistron, respectively. The first cistron of the first promoter and cistron, respectively. The first cistron of cinitiation region (TIR-L) operably linked to a nucleic acid sequence encoding an Ig light chain and the second cistron of the second promoter-cistron pair comprises a second translational initiation region (TIR-H) operably linked to a nucleic acid sequence encoding an Ig heavy chain. Upon expression of the polynucleotide in a prokaryotic host cell, light and heavy chains are folded and assembled to form a biologically active Ig. The antibody of the invention is useful for disgnosing, treating or preventing diseases or conditions associated with abnormal expression and of activity of one or more antiogen molecules e.g. lymphoid malignancies, inflammatory, angiogenic, immunologic, neuronal, glial, astrocytal, hypothalamic or other glandular disorders. The present sequence represents the amino acid sequence of an anti-tissue factor (TF) heavy
                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide comprising first and second promoter-cistron pairs, useful for diagnosing, treating or preventing diseases associated with abnormal expression and/or activity of antigens such as inflammatory
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; CD11; tissue factor; vascular endothelial growth factor; {f TF} .
                                                                                                                                                                                                                                                                                                                                                                                               chain fragment of the cistron vector paTF50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a polynucleotide, which encodes an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 20A-C; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABN86645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simmons LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-2000; 2000US-0256164P
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                                                                                                                                                                                                                                                                                        275;
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                        -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
                                                                                                                                                                                                                                                   LGKKGDTVELTCTAS -- QKKSIQFHW----- KNSNQIKILG-NQGSFLTKGPSKLNDRA
                                                                                                                                                                                                                                                                                                                                                            470 AA;
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                                                            TISADNSKNTAYLOMN-----SLRAEDTAVYYCA-------RDTAAYF
                                                                                                                                                                               ----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL--
                                                                                                                                                                                                                 LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA
                                 -----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                                                                     DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klimowaki L,
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24. .470
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                                                                                                                                                                                                                                                                                                     52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "anti-tissue factor heavy chain"
                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reilly DE,
                                                                                                                                                                                                                                                                                                       Score 1266; DB 5;
Pred. No. 1.3e-63;
                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                        Length 470;
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RESULT 93
ABP72748
ID ABP72
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XX ABP72
XX DT 11-JU
DE Anti-
XX CD18;
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chain including a heat stable enterotoxin II (STII) secretion signal. This recombinant heavy chain is produced by host cells transformed with claimed vector pxFF-773FL (see ABER2272). The plasmid contains 2 translational units that temporally separate the transcription of the antibody light (see ABP72747) and heavy chains. Expression of the light chain is under the control of the phoa promoter, while expression of the heavy chain is under the control of the inducible Tacil promoter. In an example from the invention, Escherichia coli 60H4 was transformed with pxTF-7T3FL. The light chain was expressed initially and secreted into the periplasmic space. Heavy chain production was then induced by addition of IPTG A yield of 2.6 +/- 0.3 g/l assembled F(ab')2 was obtained, compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing an antibody for treating cancer or autoimmune diseases by culturing the host cell under suitable conditions so that the light and heavy chain are expressed in a sequential fashion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                       The present sequence is that of an anti-tissue factor (TF)
                                                                                                                                                                                                                                                                                                                                                                                              Claim 56; Fig 10; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-2001; 2001US-0315209P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-tissue factor antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-278654/27.
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/note= "heat stable en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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RESULT 94
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Matches 275;
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                                                                                 16-MAY-2000; 2000US-0204518P
                                                                                                                                        04-MAY-2001; 2001WO-US014468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain
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                               (UYJE-) UNIV JEFFERSON THOMAS
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                                                                                                                                                                                                                                                                                                                                                          human rabies-immune globulin; monoclonal; virucide; heavy chai monoclonal rabies virus neutralising antibody; immunoglobulin; chain; central nervous system; CNS; prophylactic therapy; clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISADNSKNTAYLQMN-----SLRAEDTAVYYCA------RDTAAYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the monoclonal antibody from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.4%; Score 1266; DB 6; 58.8%; Pred. No. 1.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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                                                                                                                                                                                                                                                                                                                                                                  clone JA
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RESULT 95 ABU08017 ID ABU08

ABU08017

standard;

protein;

474

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426 384 366 324 306 246

209

BXGXAX

10-MAY-2003

(first entry)

Human monoclonal rabies virus

antibody heavy chain,

clone

protein

ABU08017;

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Best Local Sim
Matches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal rabies virus neutralising antibody (virucide) derived from CDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified away from deleterious contaminants. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for treating an individual exposed to a rabies virus by administering to the individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious post exposure prophylactic therapy for individuals exposed to a rabies virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the heavy chain protein of the monoclonal antibody from clone JA. The invention relates to an isolated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 23-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human monoclonal rabies virus neutralizing antibody useful for treating individual exposed to rabies virus and for preventing spread of rabies virus to central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hooper DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                  GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NKKPSNTKVD----KRVEPKS
                       SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                              KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                          DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                             CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                 CDKTHTC----PELLGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                                                                                              YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGKKGDTVELTCTAS------OKKSIQFHWKNSNQIKILGNQGSFL---TKGP
                                                                          KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                   DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                         ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTIS-RDNSKNTLYLOMN-----SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD---
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Pred. No. 1.3e-63;
12; Mismatches 71;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            containing a recombinant expression vector comprising the nucleic acid molecule encoding the antibody, and isolating the recombinant antibody expressed and treating an individual exposed to a pathogen by administering to the individual the recombinant antibody. The recombinant antibodies are useful for preventing (vaccine) and treating an individual exposed to a pathogen, e.g. rabies infection. They are also useful for the qualitative and quantitative determination of the rabies virus. The sequences presented are the antibody protein fragments, the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region. Rables is an acute, neurological disease caused by infection of the central nervous system with that shies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antibody; constant region; monoclonal antibody 57; Mab 57 variable region; Rabies; neurological disease; infection; central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant antibody comprising a constant region of Mab 57 linked a non-Mab 57 variable region, useful for treating an individual exposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-2001; 2001US-0314023P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogen; vaccine; virucide; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                        YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
                                                                                                                                                                                                                                                                                                                                                   LGKKGDTVELTCTAS-------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             them or the PCR primers used
                                                                                                    GVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS
                                                                                                                                                                                                          LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS
                                                                                                                                                                                                                                             FTIS-RDNSKNTLYLQMN-----SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD---
                                                                                                                                                                                                                                                                              SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL
                                  CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                      CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                         ----QLELQDSG----
                                                                                                                                                                                                                                                                                                               LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     52.4%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 1266; DB 5;
Pred. No. 1.3e-63;
                                                                                                                                       ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKS
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hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulir hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is
                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy clear constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide. The constant is fused to the CH2 constant region polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a binding domain-immunoglobulin fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 398; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367
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                                                             ADD25679;
                                                                                                                ADD25679 standard; protein; 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY
                                                                                                                                                                                                                                                                                                                       SLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDVWGTGTTVTVSSDQEPKSCDKTHTCPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SQLELQDSGTWTCTVLQNQKKVEFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR-----SPR----SPR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                                                                                                                                                                                                          431
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antiarthritic; immunosuppressive; antidiabetic; antithyroi neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1;
                                                                                                                              17-JAN-2001;
17-JAN-2002;
                                                                                                                                                                                                                  25-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding
  Ledbetter JA,
                                                                                                                                                                                                                                                                                                                             US2003118592-A1
                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
                                                        GENECRAFT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain-immunoglobulin fusion protein-associated protein #114.
                                                                                                       2001US-0367358P
2002US-00053530
2002US-0385691P
                                                                                                                                                                                                                  2002US-00207655
  Hayden-Ledbetter MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion
Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
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New binding domain-immunoglobulin fusion protein, useful for treating subject having or suspected of having a malignant condition or a B-cedisorder, e.g. melanoma, Grave's disease or autoimmune disease. a B-cell

WPI; 2003-801317/75.

Disclosure; SEQ ID NO 240; 157pp; English.

CC polypeptide, and an immunoglobulin heavy chain CH3 constant region (CC polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin cC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a cc mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues, where the mutated human IgG1 cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains or more cysteine residues; where contains the cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polymucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain treating a malignant condition or a B-cell disorder. -immunoglobulin fusion protein-associated protein sequence. Note: sequence data for this patent formed part of the printed specific comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy immunoglobulin hinge region polypeptide that is fused to the hinge region CH2 constant region polypeptide that is fused to the hinge region The invention relates to a binding domain-immunoglobulin comprising a binding domain polypeptide that is fused to format directly specification fusion protein chain

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15-JAN-2004

(first entry)

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Best Local S
Matches 274
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  Carter
                                                                                                   WO9222653-A1
                                                                                                                        Mus musculus
                                                                                                                                           Humanisation;
                                                                                                                                                              H52H4-160 murine anti-CD18 antibody heavy chain.
                                                                                                                                                                                   25-MAR-2003
12-MAY-1993
                                                                                                                                                                                                                                   AAR30774 standard; protein; 454
                                         14-JUN-1991;
                                                            15-JUN-1992;
                                                                                 23-DEC-1992
                     (GETH ) GENENTECH INC.
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  Presta LG;
                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                            rapid; monoclonal antibody
                                         91US-00715272
                                                            92WO-US005126
                                                                                                                                                                                                                                                                                        499
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Pred. No. 1.4e-63;
Mismatches 94;
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Matches 274
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        Domain
                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                  multivalent;
                                                                                                                                                                                                                                                                                                                                                       interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
immune disease; multiple sclerosis; Crohn's disease; skin disorders;
inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody; humanised; variable region; heavy chain; light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW85689 standard;
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                                                                                                                                                                                                                                                   CC monoclonal mouse anti-IFN gamma antibody D910; a multivalent antibody; CC or a ruminant antibody. The antibody are also useful for determining CC IISH gamma levels in a sample. Two fusion cDNA genes encoding heavy and CC light chain fusion proteins of the humanised D910 antibody were CC constructed. The light chain comprised cDNA genes encoding the mouse D910 clight chain and a human CC comprised cDNA encoding the mouse D910 light chain and a human CC comprised cDNA encoding the mouse D910 light chain leader sequence CC followed by the humanised D910 havy chain variable domain and a human CC comprised cDNA encoding the mouse D910 light chain leader sequence CC followed by the humanised D910 hight chain leader sequence. This CC was then subsequently amplified using two primers (AAX08589, AAX08590) to generate PCR-V fragment. The humanised heavy chain variable domain was CC amplified from pGEM-T-VhH using two primers (AAX08591, AAX08592) to generate PCR-VI fragment. The humanised heavy chain variable domain was CC amplified with two primers (AAX08591, AAX08592) to generate PCR-VI fragment. The humanised heavy chain constant domain was CC amplified with two primers (AAX08593, AAX08591) and then cloned CC give pGEM-T to give pGEM-Tayle. The humanised meavy chain constant domain was CC amplified with two primers (AAX08593, AAX08594) and then cloned CC give pGEM-Tch. Two separate PCR amplifications were then performed using CC pGEM-T-Ch as a template. The primers was devere AAX08598, AAX08599, to generate PCR-VIII fragment and AAX08597, AAX08598, AAX08599, CC CAAX08500 and the resulting PCR-X fragment inserted into pGEM-Tch to generate PCR-IX fragment and AAX08597, AAX08599, AAX08599, CC CAAX08500 and the resulting PCR-X fragment inserted into pGEM-GCVH to generate PCR heavy chain fusion DNA in a vector dealganted dealganted CC constant heavy chain fusion DNA in a vector dealganted dealganted CC constant heavy chain fusion DNA in a vector dealganted constant constant constant constant inserted into pGEM-GCVH.
                                                                                                                                                   Query Match
Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                                                                                   Sequence 468
                                                                                                                                                                                                                                                                                                AAX08600 and the resulting PCR-X fragment inserted into pGEMLdrVHh to generate the complete heavy chain fusion DNA in a vector designated pGEMhD9D10H. For a description of the construction of the light chain fusion cDNA see GENESEQ records AAX08573-X08584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies which bind and neutralise interferon-gamma (IFN gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including multiple sclerosis and Crohn's disease and skin disorders including bullous, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric antibody or diabody comprising the humanised variable domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New engineered antibodies which bind and neutralise interferon-gamma useful for prevention and treatment of septic shock, cachexia, immundiseases and skin disorders.
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18-JUN-1998;
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                                                 VILSOVOLVOSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L
                                                                                                LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
  KGPSKLNDRADSRRSLWD-QGNFP------LIIKNLKIEDSDTYICEVEDQKEEV 118
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                                                                                                                                                 52.4%; Score 1265.5; DB 2; 57.2%; Pred. No. 1.4e-63; tive 31; Mismatches 79;
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                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                             Antibody; humanised; variable region; heavy chain; light chain; interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                             MoTAbII fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85692 standard; protein;
                        18-AUG-1997;
                                                 14-AUG-1998;
                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSNKALPASIEKTISKAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWE
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            97EP-00870122
98EP-00870139
                                                 98WO-EP005165
                                                                                                                                                                                            468
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                          /label= Humanised)_D9D10_ScFv
                                                                                                                                                /label= Gly(3)Ser_linker
                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                       /label= Mouse_D9D10_light_chain_signal_peptide
                                                                                                                                                                             note= "Leu added
                                                                                                                                                                                                                              'note= "Humanised heavy chain variable domain of D9D10"
                                                                                                                                                                                                                    .467
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Matches 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies which bind and neutralise interferon-gamma (IFN gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including multiple sclerosis and Crohn's disease and skin disorders including bullous, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric antibody or diabody comprising the humanised variable domain of the monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody; or a ruminant antibody. The antibodies are also useful for determining IFN gamma levels in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New engineered antibodies which bind and neutralise interferon-gamma - useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 711 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 20; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAW85692.
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                                                         SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                  VSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
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                                                                                                                                                                                                                                                                                                                                                                                                                     KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC------
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Search completed: August Job time : 57.1889 secs

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Result
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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1 MNRGVPFRHLLLVLQLALLP.....DETCAEAQDGELDGLWTTDP
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COUNTRY: USA
ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08485163 Publication No. US20020098191A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
TELEPHONE:
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0 US-09-996-265-232

0 US-09-996-265-234

0 US-09-996-265-234

0 US-09-996-265-234

0 US-09-996-265-244

0 US-09-996-265-254

0 US-09-996-258-71

1 US-10-177-023-133

4 US-10-159-006-30

1 US-09-996-288-224

1 US-09-996-288-224

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US-09-996-288-254
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Sequence 231, App
Sequence 233, App
Sequence 244, App
Sequence 244, App
Sequence 252, App
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Sequence 253, App
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                                                                                                                               ; TYPE: PRT
; ORGANISM: homo
US-09-766-995-2
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US-09-766-995-2
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JFW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 432
TABLE DATE:
THE PATENTIAL OF THE PATENTIAL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09766995
Patent No. US20020052481A1
Query Match
Best Local Similarity
Matches 405; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDENNESS: unknown
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MOLECULE TYPE: prote:
ORIGINAL SOURCE:
ORGANISM: homo sap:
CELL TYPE: lymphoc:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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87.9%;
ilarity 91.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 391-0525
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91.2%;
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Score 2122; DB 9;
Pred. No. 1.9e-141;
8; Mismatches 5;
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Pred. No. 1.9e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
                                                               Length 432;
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Indels

26;

Gaps

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Publication No. US20020098191A1
GENERAL INFORMATION:
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooper &
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CITY: New York
STATE: New York
COUNTRY: USA
TYPE: amino acid
STRANDEDNESS: unb
TOPOLOGY: unknown
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1185 Avenue of the Americas
   unknown
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; Sequence 4, Application US/09766995
; Patent No. US20020052481A1
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOLETY-CONJUGATED CD4
TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 2048/41215-CB/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/766,995
; CURRENT APPLICATION NUMBER: US/09/766,995
; CURRENT FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: homo sapians
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; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-485-163-5
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US-09-766-995-4
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                                                  Query Match
Best Local S
Matches 409
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Best Local Similarity 77.3%;
Matches 409; Conservative
                                                              Local Similarity
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            MNRGVPFRHLLIVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                  Conservative
                                                           86.4%;
77.3%;
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                                                Score 2085; DB 9;
Pred. No. 9.9e-139;
9; Mismatches 13;
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Pred. No. 9.9e-139;
9; Mismatches 13;
                                                                           Length
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US-09-939-537-33
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TITLE OF INVENTION: TARGETED CYTOLYSIS
CELLS BY CHIMERIC (
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                          IOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1991
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW
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                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDSDGSFFLYSKLTVDKSRWQQQNVFSCSVMHEALHNHYTQKSLSLSSPG 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
NAME: Elbing,
                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTKGÓPREPÓVYTLPPSREEMTKNÓVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM
                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
Karen
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CD4 RECEPTOR- BEARING CELLS
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STRANDEDIESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-09-939-537-33
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                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-10-404-724-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10404724 Publication No. US20030203447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         SOFTWARE: 1
                                                                                                                                      Matches
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/404,724
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/368,530
PRIOR ETLING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOTWITZ, Arnold H.
TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 13698US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
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LKWMGWINTYTEEPTYGDD------FKGRFAFSLETSASTANLQINNLKSEDTATYF 114
                                                                  LLFLMAAAQSAQAQIQLVQSGPELKKPGETVKISCKAS---GYTFTKYGMNWVKQAPGKG
                                                                                                LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                              -----SFLTKGPSKLNDRADSRRSLWDQGNFP------LIIKNLKIEDSDTYI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE
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58.1%;
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98.0%;
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                                                                                                                                                    Score 1291.5; DB 12; Pred. No. 7.9e-83;
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Pred. No. 1.8e-86;
                                                                                                                                    Mismatches
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                                                                                                                                    78;
                                                                                                                                   Indels 105;
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                                                                                                                                                                   Length 465
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                                                                                                                                   Gaps
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APPLICANT: Large Scale Biology
APPLICANT: Reinl, Stephen J.
APPLICANT: Redwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/10/679,620
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOSTWARE: Patentin version 3.2
SEG ID NO 64
LENGTH: 713
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US-10-679-620-64
US-10-679-620-64
; Sequence 64, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     Best Local Sim
Matches 275;
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                           Local Similarity
   435
                                 173
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                                                                                                                                                                       77
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TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                 --QLELQDSG-----
                                                                                                                                     KGRFTISRDN-DKNALYLQMNSLKSEDTAMYYC----ARRSEFYYYGNTYYYSAMDYWG
                                                                                                                                                                   NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                                                                                                                                                                                                                                       LGKKGDTVELTCTAS------QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
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                                                                                                                                                                                                       LVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEW-----VATIGSRGTY-THYPDSV 320
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                                                                 QGASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                   QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                     53.4%; Score 1289; DB 16;
59.3%; Pred. No. 2e-82;
70. Mismatches 81;
                                ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                                           Length
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CURRENT APPLICATION UMBER: US/10/679,620
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.2
SEQ ID NO 62
LENGTH: 715
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-679-620-62
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Publication No. US20040110930A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reinl, Stephen J.
APPLICANT: Edwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.3 Matches 275; Conservative
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611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 LGKKGDTVELTCTAS------QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKKLEW-----VATIGSRGTY-THYPDSV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                     PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                             EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                       THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                             TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                                                                                   --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                     QASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                   KGRFTISRDN-DKNALYLQMNSLKSEDTAMYYC----ARRSEFYYYGNTYYYSAMDYWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                     THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                             QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                                                                       EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: KODALENTIN 1.71
SEQ ID NO 14
LENGTH: 437
TYPE: PRT
ORGANISM: Homo sapiens
US-10-363-427-14
           US-10-412-406-32
Sequence 32, Application US/10412406
Publication No. US20040058394A1
GENERAL INFORMATION:
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US-10-363-427-14
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APPLICANT: CHUNG, Yong Hoon
APPLICANT: HAN, Ji Woong
APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: YIM, Soo Bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/10363427 Publication No. US20030195338A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: BIOGEN, INC
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                                                                                                                                                                                                              GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
                                                                                                                                                                                                                                                        NKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESN
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; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo 9
US-10-412-406-32
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APPLICANT: SALDHANA, JOSE W.
APPLICANT: SALDHANA, JOSE W.
FIITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINA10CN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
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Best Local
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                                                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
                                                                                                                                                                                                                                                                                 DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVD
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DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                           DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                        GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                               DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, JOSE W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANT;
; FILE REFERENCE: BINALOCN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10

ANTIBODIES

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Sequence 7, Application US/10435299
Publication No. US20040052783A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Link, Brian
APPLICANT: Cingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Foe, J Yun
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
FILE REFERENCE: 05892-0176-CNUS04
CURRENT APPLICATION NUMBER: US/10/435,299
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 09/618,380
PRIOR APPLICATION NUMBER: US 08/397,411
PRIOR APPLICATION NUMBER: US 07/859,583
PRIOR APPLICATION DATE: 1992-03-27
NUMBER OF SEQ ID NOS: 14
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PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR PILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 4852
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US-10-435-299-7
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Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4513 WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 4572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4473 ISRDNAKUSLY-----LQMSSLRAEDTAVYYCAREE------NGNFYYFDY 4512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4414 LVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSY-TYYPDSVKGRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 -DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQPREPQVYTLPESRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 4746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GOSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.3%; Score 1285.5; DB 12; Length 59.0%; Pred. No. 4.1e-81; vative 29; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 446
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.1%;
Best Local Similarity 59.8%;
Matches 274; Conservative 25
408
                  394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                   ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                              TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                             CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                         QSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                                                                                                                                                                                                                                                                                                                           VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                                                                                                                                                                                                                                                          LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----QLEL
                                                                                                                                                                                                                                                                                                                                                                                                                        --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS
                                                              YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                           QDSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                                          KDTSKNOVSLKLNSLTAADTAVYYC-----ARNDRYAMDYWGQGTLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1282.5;
Pred. No. 3.26
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445
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RESULT 13

US-10-363-427-18

I Sequence 18, Application US/10363427

Publication No. US20030195338A1

GENERAL INFORMATION:

APPLICANT: HAN, Ji Woong

APPLICANT: HAN, Ji Woong

APPLICANT: HAN, Ji Woong

APPLICANT: LEE, Hye Ja

APPLICANT: KIM, Jin Mi

APPLICANT: KIM, Jin Mi

APPLICANT: KIM, Joo Bin

ITITLE OF INVENTION: Concatametric Immunoadhesion

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/363,427

CURRENT APPLICATION NUMBER: US/10/363,427

CURRENT FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 52

SOFTWARRE: Kopatentin 1.71

SEQ ID NO 18

LENGTH: 617

TYPE: PRT

ORGANISM: Homo Bapiens

US-10-363-427-18

Query Match 53.1%; Score 1282.5; DB 14; Length 617; Best Local Similarity 64.5%; Pred. No. 4.9e-82; Matches 272; Conservative 22; Mismatches 63; Indels 65;

Gaps

11;

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CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: KOPAtentIn 1.71
SEQ ID NO 22
LENGTH: 617
TYPE: PRT
ORGANISM: Homo Bapiens
US-10-363-427-22
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US-10-363-427-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/10363427 Publication No. US20030195338A1 GENERAL INFORMATION:
                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MeDexGen Inc.
APPLICANT: CHUNG, Yong Hoon
APPLICANT: HAN, Ji Woong
APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: YIM, Soo Bin
TITLE OF INVENTION: Concatametric Immunoadhesion
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615
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 326
                             143
                                                             273 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
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                                                                                                                                                                                                          Similarity
CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
                            LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVE
                                                                                            IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ------SLTLT 142
                                                                                                                             DDIKWEKTSDKKKIAQFRKEKE-----TFKEKDTYKLFK-----NGTL 272
                                                                                                                                                        DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                          53.1%; Score 1282.5; DB 14; Length 617; 64.5%; Pred. No. 4.9e-82;
                                                                                                                                                                                           22;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                         63; Indels
                                                                                                                                                                                         65;
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APPLICANT: Power, Scott D.

APPLICANT: Wang, Huaming
APPLICANT: Ward, Michael
TITLE OF INVENTION: Production of Functional Antibodies in
TITLE OF INVENTION: Production of Functional Antibodies in
TITLE OF INVENTION: Pilamentous Fungi
FILE REFERENCE: GC741-2
CURRENT APPLICATION NUMBER: US/10/418,836
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US 60/373,889
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-09-18
PRIOR PPLICATION NUMBER: US 60/411,540
PRIOR PRIOR APPLICATION NUMBER: US 60/452,134
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 60/452,134
PRIOR APPLICATION NUMBER: US 60/452,134
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 60/411,537
PRIOR PRIOR DATE: 2002-09-18
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-10-418-836-38
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US-10-418-836-38
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Best Local :
                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                      y Match 53.1*; Score 1282.5; DB 15; Length 972;
Local Similarity 59.8*; Pred. No. 8.7e-82;
hes 274; Conservative 25; Mismatches 80; Indels 79;
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QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                            QDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
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CURRENT APPLICATION NUMBER: US/10/418,836
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US 60/373,889
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US 60/411,540
PRIOR APPLICATION NUMBER: US 60/452,134
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 60/452,134
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 60/411,537
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SOFTWARE: PASTSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PASTSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 39
LENGTH: 975
TYPE: PAT
ORGANISM: Artificial Sequence
PEATURE:
COTHER INFORMATION. Fusion Protein
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US-10-418-836-39
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Publication No. US20040018573A1
GENERAL INFORMATION:
APPLICANT: Power, Scott D.
APPLICANT: Wang, Huaming
APPLICANT: Ward, Michael
TITLE OF INVENTION: Production of Functional Antibodies
FILE REFERENCE: GC741-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.1%; Score 1282.5; DB 15; Length 975; Best Local Similarity 59.8%; Pred. No. 8.7e-82; Matches 274; Conservative 25; Mismatches 80; Indels 79; Gaps
274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
                                                757
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                                              CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 816
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                                                                           ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                           QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP 756
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53.1%; Score 1281.5; DB 12; Length 465; ity 57.7%; Pred. No. 4e-82; servative 24; Mismatches 79; Indels 105; Gaps 13;	h Similaı 84; Cor	Query Match Best Local Similarity Matches 284; Conservat	
SLTCLVKGFYPSDIAVEWESNGG	34 YTLPPR	877 YTLPPSRDELTKNQV 877 YTLPPSRDELTKNQV 877 YTLPPSRDELTKNQV 394 KLTVDKSRWQQGNVF	US STATE OF THE CONTROL OF THE CONTR
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US-09-747-669-3
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US-10-656-769-32
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APPLICANT: Witte, Alison
APPLICANT: Witte, Alison
APPLICANT: Weina, Chris
APPLICANT: Wong, Lu Min
APPLICANT: Wong, Lu Min
APPLICANT: Olan, Xueming
TITLE OF INVENTION: Therapeutic Human Anti-IL-IR Monoclonal Antibody
FILE REFERENCE: 01,1554
FILE REFERENCE: 01,1554
CURRENT APPLICATION NUMBER: US/10/656,769
CURRENT APPLICATION ON 199-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
**THERMIN ACT
                                                                    Sequence 3, Application US/09747669
Patent No. US20020122807A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 467
TYPE: PRT
ORGANISM: Homo &
S-10-656-769-32
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Best Local Similarity
APPLICANT: Dan, Michael D.
APPLICANT: Saleh, Mansoor
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: 485 THAT SPECIFICALLY DETECT CANCER CELLS,
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                                                                                                                                                                                            TQKSLSLSPG
                                                                                                                                                                                                                  TQKSLSLSPG
                                                                                                                                                                                                                                                                                    IAVEWESNGQPENNYKTTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMGIIHPGASDTRYSPSFQGQVTISADNSNSATYLQW------SSLKASDTAMYFCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIKILGNQGSFLTKGPS---KLNDRADSRRSL----WDQGNFPLIIKNLKIEDSDTYICE
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                                                                                                                                                                                                                                                               IAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
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57.1%; Pred. No. 5.2e-82;
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   NUCLEOTIDES
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Sequence 3, Application US/10290703

Publication No. US20030118593A1

GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Saleh, Mansoor
ITILE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
ITILE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF
ITILE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF
ITILE OF INVENTION: AND DETECTION OF CANCERS
ITILE REFERENCE: 316082001002

CURRENT APPLICATION NUMBER: US/10/290,703

CURRENT FILING DATE: 2002-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 316082001001

CURRENT APPLICATION NUMBER: US/09/747,669

CURRENT FILING DATE: 2002-04-08

PRIOR APPLICATION NUMBER: US 09/111,286

PRIOR FILING DATE: 1998-07-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 476

TYPE: PRT

ORGANIEM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-3
                                                                                                                                                                                                                                     RESULT 20
US-10-290-703-3
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Matches 280; Conserv
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGWMNPNSGK-----TGYAQKFQGRVTMTRNTSIRTAY-MELSGLRSEDTAVYFCA
                                                                                                                                                                                                                                                                                                                                               HYTOKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLNWVRQAPGQGLEW
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Pred. No. 5.3e-82;
17; Mismatches 91;
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; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASCSEQ for Windows Version 4.0
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 476
                                                                                                                                                                                                                                                                                             RESULT 21
US-10-378-567-2
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; OTHER INFORMATION: Synthetic construct US-10-290-703-3
                                                                                                                                                                                                                                     Sequence 2, Application US/10378567 Publication No. US20040006208A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 280; Conserv
                                                                                            APPLICANT: KARPUSAS, MICHAEL
APPLICANT: HSU, YEN-MING
APPLICANT: TAYLOR, FREDERICK R.
APPLICANT: TAYLOR, FREDERICK R.
APPLICANT: ZHENG, ZHONGLI
TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY
TITLE OF INVENTION: CD154, AND USE THEREOF IN DRUG DESIGN
FILE REFERENCE: A096CON1
PRIOR APPLICATION NUMBER: PCT/US01/27352
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/276,452
                                                       CURRENT APPLICATION NUMBER: US/10/378,567
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGWMNPNSGK-----TGYAQKFQGRVTMTRNTSIRTAY-MELSGLRSEDTAVYFCA 116
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Sequence 344, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
FILE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT PILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SOPTWARE: Patentin version 3.0

SEQ ID NOS: 426
LENGTH: 492

TYPE: BRT
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PRIOR APPLICATION NUMBER: 60/229,93
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 448
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US-10-207-655-344
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                                  US-10-207-655-344
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Best Local Similarity
Matches 275; Conserv
Query Match
                                                FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: humanized 5c8 heavy chain amino acid
                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDKTHTC-----PBLLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
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                                                                                                                                                                                                                                                                                                                                                                                                                  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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Pred. No. 5.3e
31; Mismatches
 Score 1279;
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Length 492;
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APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
FILE OF INVENTION: No. US20040005560A1el full length cDN
FILE REFERENCE: H1-A0106
CURRENT APPLICATION UMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4292
LENGTH: 470
TYPE: PRT
ORGANISM: Homo Bapiens
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US-10-108-260A-4292
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Publication No. US20040005560A1
GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                        Similarity
                                   FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTL 169
                                                                         G-RPNYAQKFQDRVTISADESSSI-----VYMDLDRLTIEDTAIYFCAI------LLE
                                                                                                           GNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                             QVQLVQSGTE----VKKPGSSVKVSCKASGGSFSSYVFTWVRQAPGEGLEWMGSIPIL
                                                                                                                                                                               QLALLPAATQGNKVVLGKKGDTYELTCTAS--QKKSIQFHWKN-----SNQIKIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYCA----RIHFDYWGQGVMVTVSSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTCTVLQNQKKVEFK----IDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVQ-CRSPRGKNIQ------GGKT------LSVSQLELQDSGT
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   HEVRALFD-HWGQGTLVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF
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                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                 52.9%; Score 1277.5; DB 15; Lengt 58.8%; Pred. No. 7.8e-82; ative 31; Mismatches 77; Indels
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US-10-207-655-345

US-10-207-655-345

; Sequence 345, Application US/10207655

; Publication No. US20030118592A1

; GENERAL INFORMATION:
    APPLICANT: Ledbetter, Jeffrey A.
    APPLICANT: Hayden-Ledbetter, Martha S.
    TITLE OF INVENTION: BINDING DOMAIN-INMUNOGLOBULIN FUSION PROTEINS
    FILE REFERENCE: 390069.401C1

; CURRENT APPLICATION NUMBER: US/10/207,655

; CURRENT FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 426

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 345

LENGTH: 543
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 52.9%; Score 1277; DB 14; Local Similarity 55.8%; Pred. No. 1e-81; nes 279; Conservative 33; Mismatches 92;
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                                                                                                                                               WTCTVLQNQKKVEFK-----IDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPK 231
                                                                                                                                                                                                                                                                          GSGTKLEIKRGGGGSGGGGSGGGGSQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD 177
                                                                                                                                                                                                                                                                                                                                               --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120
                                                                                                                                                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE-----
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                                                                             PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
                                                                                                                                                                                                  GVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM 237
                                                                                                                                                                                                                                        SVQ-CRSPRGKNIQ------GGKT-------LSVSQLELQDSGT 181
                                                                                                                                                                                                                                                                                                              ----VEDQK-----EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                     MSRGVD-----IVL------TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDPEVKFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 351
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                    TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT
                                                                                                                              YYCA-----RIHFDYWGQGVMVTVSSDLEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK
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                                                        PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
DB 14;
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Gaps

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Sequence 25, Application US/09740002

Patent No. US20020001798A1

GENERAL INFORMATION:

APPLICANT: BRAMS, PETER

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: NEGRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0275759

CURRENT APPLICATION NUMBER: US/09/740,002

CURRENT APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 08/488,376

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27

SOFTMARE: Patentin Ver. 2.1

SEQ ID NO 25

LENGTH: 475
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US-09-740-002-25
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ORGANISM: Homo sapiens
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 HYTQKSLSLSPG 431
                                                                                                                              NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                           NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSNQIKILGN-----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC 109
                                                        SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                         NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
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                                   SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                                                                                                                            -----KTLSVS-----TWTC 184
                                                                                                                                                                                                                                                                                                                                                                                                -----ARVGLYDINAYYLYYLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA 168
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Sequence 25, Application US/10325698

| Publication No. US20040076631A1
| GENERAL INFORMATION:
| APPLICANT: BRAMS, PETER |
| APPLICANT: MORROW, PHILLIP |
| TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES |
| TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR |
| TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF |
| FILE REFERENCE: 037003-0275759 |
| CURRENT APPLICATION NUMBER: US/09/140,002 |
| PRIOR APPLICATION NUMBER: US/09/740,002 |
| PRIOR APPLICATION NUMBER: 09/335,697 |
| PRIOR APPLICATION NUMBER: 09/335,
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US-10-325-698-25
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Matches 281
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                                                                                                                                        SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                                                                                                                                                                                                   RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                              NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
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HYTQKSLSLSPG
                                                    HYTOKSLSLSPG 431
                                                                                                                                                                                                                    NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                                                                                                                                                                   RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQEWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ARVGLYDINAYYLYYLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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57.1%; Pred. No. 9.3e-82;
ative 27; Mismatches 87; I:
  474
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Sequence 41, Application US/10138727A

Publication No. US20030157054A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-ming
APPLICANT: Qian, Susan

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REPERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/10/138,727A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
LENGTH: 579
Type: PAT
                                                                                                                             RESULT 28
US-10-334-235-38
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                  Sequence 38, Application US/10334235
Publication No. US20040131591A1
GENERAL INFORMATION:
APPLICANT: Oxfard Biomedica (UK) Ltd.
APPLICANT: Kingsman, Alan
APPLICANT: Bebbington, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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ORGANISM: Artificial sequence
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Kingsman, Alan
Bebbington, Chr.
Carroll, Miles
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                                                                                                                                                                                                     HLLLDLQ 468
                                                                                                                                                                                                                                        ETCAEAQ 442
                                                                                                                                                                                                                                                                            SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLE
                                                                                                                                                                                                                                                                                               SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQLD
                                                                                                                                                                                                                                                                                                                                                                      PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                       EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --QLELQDSG-----
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PRIOR APPLICATION NUMBER: US 100060,585
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/GB00/04317
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 600
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RESULT 29
US-10-320-231A-79
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lamikandra, Abigail TITLE OF INVENTION: VECTOR SYST
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                                                                                        DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                          GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQD------YNSPPTFG
                                                                                                                                                                               GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
                                                                                                                                                                                                                     GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                           DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                              DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
                                                                                                                                                                                                                                                                                                                                                               VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTKLEIKRASTKG---PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOGNKVVLGKKGDTVELTCTASOKKSIOFHWKNSNQIKILGNOGSFLTKGPSKLNDRADS
                                                                DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                   ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
                                                                                                                                             GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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ilarity 59.4%;
Conservative 1
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Pred. No. 1.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
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Sequence 79, Application US/10320231A
Publication No. US20030194405A1
GENERAL INFORMATION:
APPLICANT: Neben, Steven
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Tomkinson, Adrian
TITLE OF INVENTION: Antibody Inhibiting Steven
TITLE OF INVENTION: Treatment Of Asthma
TITLE OF INVENTION: Treatment Of Asthma
FILE REFERENCE: 7430*163

Stem

Cell

Factor

Activity

And

Use

488

428

CURRENT APPLICATION NUMBER: US/10/320,231A

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Sequence 6, Application US/10150475A

Publication No. US20030103985A1

GENERAL INFORMATION:
APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cyctoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/121
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR FILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6
LENGTH: 444
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US-10-150-475A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 277
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PRIOR APPLICATION NUMBER: US 60/342,174
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.2
SEQ ID NO 79
                OTHER INFORMATION: Description of Artificial Sequence: Humanised OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO:
                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial
                                                                                                   TYPE: PRT
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Local Similarity 59.2%;
tes 277; Conservative 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VWQQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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; Pred. No. 1.2e-81; 
27; Mismatches 67; Indels 97;
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                                                                                                                                                                                       ; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6
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                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 6
                                                                                                            Query Match
Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Hei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 275; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Compositions and methods for treating TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjuga FILS REFERENCE: 1/1414 CURRENT APPLICATION NUMBER: US/10/704,522 CURRENT FILLING DATE: 2003-11-07
                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                               LENGTH: 444
TYPE: PRT
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NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                                     LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI
                                                                      LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
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                                                                                                              Conservative
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                                                                                                                             52.8%;
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                                                                                                            Score 1273.5; DB
Pred. No. 1.4e-81;
Pred. No. 1.6e-81;
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Pred. No. 1.4e
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APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Chemotherapeutic Agents
FILE REFERENCE: 1/1383
CCURRENT APPLICATION NUMBER: US/10/645,215
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: EP 02 018 686.2
PRIOR APPLICATION NUMBER: EP 0303-08-21
PRIOR FILING DATE: August 21, 2002
PRIOR FILING DATE: August 21, 2002
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
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US-10-645-215-6
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Matches
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APPLICANT: Adolf, Guenther
APPLICANT: Baum, Anke
APPLICANT: Heider, Karl-He
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                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                        Similarity
                                                                                                        S-RDNAKNSLYLOMN-----SLRAEDTAVYYCARQ------GLD-----YWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
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                                                                      QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS----
                                                                                                                                           NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                                                                                                                                                                              LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70
                                                                                                                                                                                                                LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFFLYSKLTYDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
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 --QLELQDSG---
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                      52.8%;
59.3%;
                                                                                                                                                                                                                                                                      Score 1273.5; DB Pred. No. 1.4e-81;
                                                                                                                                                                                                                                                     Mismatches
--TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                       Length 444;
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GENERAL INFORMATION:

APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT APPLICATION NUMBER: 09/335,697
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
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; TYPE: PRT
; ORGANISM: Homo s
US-09-740-002-27
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US-09-740-002-27
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Patent No. US20020001798A1
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Best Local :
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                                                                                                      EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
                                                                                                                                                              FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 235
                                                                                                                                                                                                                --KTLSVS-----TWTCTVLQNQKKV 193
                                                                                                                                                                                                                                                          DSFYLF----YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 177
                                                                                                                                                                                                                                                                                                  VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------ 166
                                                                                                                                                                                                                                                                                                                                                                                   ----GNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKIL---
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VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                        VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
                                                                                                                                                                                                                                                                                                                                           ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                  LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.8%; Score 1273.5; DB 9; Length 475; ilarity 57.1%; Pred. No. 1.5e-81; Conservative 29; Mismatches 99; Indels 79;
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Sequence 27, Application US/10325698

Publication No. US20040076631A1

GENERAL INFORMATION:
APPLICANT: BRAMS, PETER

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0275759

CURRENT APPLICATION NUMBER: US/10/125,698

CURRENT EPILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: US/09/740,002

PRIOR APPLICATION NUMBER: US/09/740,002

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 08/488,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-698-27
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US-10-325-698-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.8%; Score 1273.5; DB 16; Length 475; Best Local Similarity 57.1%; Pred. No. 1.5e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
                                           352
                                                                                   309
                                                                                                                                 292
                                                                                                                                                        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                   236 NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                194 EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                178 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 235
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  369
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                                                                                                                                                                                                                                                                                                                                                                                                                                      118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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  NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                           SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                      SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                               VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
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; ORGANISM: Homo
US-10-683-255-6
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US-10-683-255-6
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Best Local Similarity
Matches 276; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/49, 846
PRIOR FILING DATE: 2000-02-07
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kavanaugh, William M.
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-INMUNOGLOBULIN
FILE REFERENCE: PP01474.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/683,255
CURRENT FILING DATE: 2003-10-10
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437
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                                                                                                                                                                                                                                                                                                                                        164 -- QGGKTLSVSQLELQDSGTWTC-----TVLQNQKKVEFKIDIVPCP---
                                                                                                                                                                                                                                                                                                                                                                                                                      123 FGLTANSDTHLLQGQSLTLTLESPP------GSS-----PSVQCRSPRGKNI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
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                                                                                               ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
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                                                                       ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO
                                                                                                                                                                                   SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                             EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                 ----APEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                      TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                               SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
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Pred. No. 1.6
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RESULT 36
US-10-683-255-4
; Sequence 4, Ap
; Publication No

Application US/10683255 No. US20040063910A1

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APPLICANT: Kavanaugh, william M.
APPLICANT: Ballinger, Marcus
ITILE OF INVENTION: FIBROBLAST GROWTH FACTOR
ITILE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU;
FILE REFERENCE: PP01474-101
CURRENT APPLICATION NUMBER: US/10/683,255
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR FILING DATE: 2000-02-07
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 4
APPLICANT: Kavanaugh, William M.
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: PP01474.101
CURRENT APPLICATION NUMBER: US/10/683,255
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR APPLICATION NUMBER: 09/199,846
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR FILING DATE: 1999-02-08
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US-10-683-255-2
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                                                                                                                                                                                                                                   Sequence 2, Application US/10683255 Publication No. US20040063910A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 276; Conserv
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; NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
; LENGTH: 622
; TYPE: PRT
; ORGANIEM: Homo sapiens
US-10-683-255-2
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                                                                                                                       ; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4282
                                                                                                                                                                                                                                                                                                                                                                                   US-10-108-260A-4282
                                                                                                                                                                                                                                                                          Sequence 4282, Application US/10108260A Publication No. US20040005560A1 GENERAL INFORMATION: APPLICANT: HELLX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20040005560A1 FILE REFERENCE: H1-A0106
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4282
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Best Local Similarity
Matches 276; Conserv
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                                                                                     Query Match
                                                   Local Similarity
nes 280; Conserv
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16 LALLPAATQGNKVV-----LGKKGDTVELTCTASQKKSIQF-----HKNSNQIKILGNQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIKILGNQGSFLTKGP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIVP----CPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLESRG 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFVPSDIAVEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLTANSDTHLLQGQSLTLTLESPP------GSS-----PSVQCRSPRGKNI- 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                   Conservative
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                                                                     52.7%;
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57.0%; Pred. No. 2.1e-81;
rative 31; Mismatches 86; Ii
                                                                                                                                                                                                                                                                                              US20040005560Alel full length cDNA
                                                     28;
                                                 Score 1272.5; DB 15;
Pred. No. 1.8e-81;
8; Mismatches 84; I
                                                     Indels 95; Gaps
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; FEATURE:
, NAME/KEY: Misc feature
; LOCATION: 20
; OTHER INFORMATION: Xaa may be glutamine or glutamic
US-10-660-128-12
                                                                                                                                                                                                                                                                                                          FILE REFERENCE: P1245R1P2B

CURRENT APPLICATION NUMBER: US/10/660,128

CURRENT FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US/09/584,166

PRIOR APPLICATION NUMBER: US/09/584,166

PRIOR PAPLICATION NUMBER: US/09/322,875

PRIOR PILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: US/09/237,299

PRIOR FILING DATE: 1999-01-25
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  Query Match
Best Local S
Matches 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/10660128
Publication No. US20040120947A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Mim, Kyung Jin
TITLE OF INVENTION: DR4 Antibodies and Uses Thereof
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                           OTHER INFORMATION: Sequence is
                                                                                                                                                                                                                                                             LENGTH: 476
  Local Similarity 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
52.7%; Score 1272; DB 16; Length 476; 60.4%; Pred. No. 1.9e-81; ative 29; Mismatches 82; Indels 68
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Gaps
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12;
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APPLICANT: Rettig, Wolfgang J.

TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890002

CURRENT APPLICATION NUMBER: US/10/159,006

CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/301,593
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: US 98107925.4
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: US 60/086,049
PRIOR APPLICATION NUMBER: US 60/086,049
PRIOR APPLICATION NUMBER: US 60/086,049
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 18
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US-10-159-006-18
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                                                                                                                                                               Query Match 52.7%; Score 1271.5; D
Best Local Similarity 59.0%; Pred. No. 2e-81;
Matches 271; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/10159006 Publication No. US20030143229A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Park, John E.
                                                                                                                                                                                                                                                                                        LENGTH: 45
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 SLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 SSPSVQCRSPRGKNIQGG------KTLSVS------QLELQDSG--
                                         87
  70
                                                                                                                      30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 QVFLKMNSLQTDDTAMYYCAREGEFD-----YYGSSLLS-YHSMNFWGQGTSVTVSSAKT 149
                                                                                                                                                                                                                                                                                                                453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 SLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAVGSTNYNSALMSRLSISKDNSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 TVELTCTAS--OKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSL-WDQGNF
                                W----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ---GQSLTL 141
TVGKSSSTAYMELRSLTSEDSAVYFC-----ARRRIAYGY---DEGHAMDYWGQGTSV
                                                                               LVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLEWIGGINPNNGIPNYNQKFKGRATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garin-Chesa, Pilar
Bamberger, Uwe
Leger, Olivier
Saldanha, Jose W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLIIK--NIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLTLESPPG
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APPLICANT: HOTWILZ, Arnold H.
APPLICANT: HOTWILZ, Arnold H.
TITLE OF INVENTION: Methods and Materials For Invention Polypeptides
FILE REFERENCE: 13698US01
CURRENT APPLICATION NUMBER: US/10/404,724
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/368,530
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
LENGTH: 465
TYPE: PRT
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US-10-404-724-25
i Sequence 25, Application US/10404724
publication No. US20030203447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-10-404-724-25
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                      237
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                                                                                     WTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                      YICNV--NHKPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL
                                                                                                                            GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
                                                                                                                                                                G------T
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                                                                                                                                                                                                                                                                            LEWMGWINTYTEEPTYGQKF------QGRFTFTLDTSTSTAYLEISSLRSEDTA
                                                                                                                                                                                                                                                                                                            -----SFLTKGPS---KLNDRADSRRSLWDQGNFP-----LIIKNLKIEDSD
                                                                                                                                                                                                                                                                                                                                                LIFLMAAAQSAQAQIQLVQSGAEVKKPGESVKISCKAS---GYTFTKYGMWWVRQAPGQG
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57.2%; Pred. No. 2e-81;
tive 23; Mismatches
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US-10-207-655-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
Matches 275; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE:
NAME KEY: SITE
LOCATION: (1)..(265)
OTHER INFORMATION: MOUSE A
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 499
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (266).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MOUSE-HUMAN HYBRID FUSION PROTEIN
 306
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                                                                                                                                                                                                                                                                                                                               82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137
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                                                                                                                                                                                 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252
                                                                                                                                                                                                                                                                                                                                                                                                     SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                     TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
                                     CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
                                                                CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
                                                                                                             FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                            IDI-----VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKFKDTLMISRTPEVT 245
                                                                                                                                                                                                                                                                                             ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR------SPR------ 159
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                                                                                                                                                                                                                                                         SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192
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                                                                                                                                                                                                                   ------GKNIQGGKTLSV------SQLELQDSGTWTCTVLQNQKKVEFK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1271.5; DB 14
Pred. No. 2.2e-81;
Pred. No. 2.3e-81;
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RESULT 43
US-10-207-655-148
y Sequence 148, Application US/10207655
y Publication No. US20030118592A1
y GENERAL INFORMATION:
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FEATURE:
; OTHER INFORMATION: Mouse-Human hybrid fusion protein
US-10-207-655-148
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Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 148
LENGTH: 499
TYPE: DET
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                                                                    WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                           CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
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                                                                                                                                                                                                                            FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                                                                                                                                         IDI-----PELLGGPSVFLFPPKPKDTLMISRTPEVT
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                                                                                                                                                                                                                                                                                                             -----SQLELQDSGTWTCTVLQNQKKVEFK
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                                                     WESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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Pred. No. 2.2e-81;
""Gmatches 93;
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Sequence 15, Application US/10053530

Publication No. US2003013393A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Hayden-Ledbetter, Martha
APPLICANT: Hayden-Ledbetter, Martha
TITLE OF INVENTION:
FILE REFERENCE: 390069.401
CURRENT APPLICATION NUMBER: US/10/053,530
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION UNMBER: US 09/765,208
PRIOR APPLICATION UNMBER: US 09/765,208
PRIOR FILING DATE: 2001-01-17
INUMBER: US 09/765,208
INUMBER: DETERMINE PATENTIN VERSION 3.0

SOFTWARE: PatentIn version 3.0

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Matches 275;
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OTHER INFORMATION: MOUSE-HUMAN HYBRID FUSION PROTEIN
NAME/KEY: SITE
LOCATION: (1)..(265)
OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV: 2H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: DOMAIN
LOCATION: (266)..(499)
OTHER INFORMATION: HUMAN IGG1 WILD TYPE HINGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                              WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                        CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
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                                   LSLSPG 431
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LSLSPG
                                                                          WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                   CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
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498
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56.6%;
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RESULT 45 US-09-948-429B-12

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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1...
CURRENT APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/09/948,429B
FILING DATE:
PRIOR APPLICATION NUMBER: US/09/948,429B
FILING DATE: US/09/948,7550
FILING DATE: US/09/948,7550
FILING DATE: US/09/948,916
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 012712-131
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
FILEFAX: 703-836-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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STATE: VA
COUNTRY: USA
      318
                                 274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
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TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                             CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                                                         QDSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------QLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY----NNWFDVWGPGVLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
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C 216	OV 177 ODSGTWTCTVLONOKKVEFKIDIVPCPAPEPKSCDKTHTC	_	
AVL 203	Db 144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL		
-QLEL 176	QY 143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQI		
	; 90 IST		
TLT 142	Qy 86 LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT		
: : 2VT 89	Db 30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT		
RS 85	Qy 30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS		
98 11;	Query Match 52.7%; Score 1271; DB 12; Length 476; Best Local Similarity 59.8%; Pred. No. 2.3e-81; Matches 274; Conservative 29; Mismatches 87; Indels 68; Gaps		
	<pre>HARACTERISTICS: 176 amino acids amino acid (: linear TYPE: protein 12</pre>		
	TELEPHONE: 703-836-6620 TELEPAX: 703-836-2021 INFORMATION FOR SEO ID NO: 12:		
	REFERENCE/ TELECOMMUNIC		
	_ ::		
	141		
	FILING DATE: US/09/758,173 CLASSIFICATION:		
	SOFTWARE: PatentIn R CURRENT APPLICATION DAT		
	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS		
	COMPUTER REA		
	COUNTRY: ZIP: 22		
	CITY: Alexandria STATE: VA		
	ADDRESSEE: F		
	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES		
USE THEREOF AS	TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND TITLE OF INVENTION: IMMUNOSUPPRESANTS"		
EREOF.	TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS		
	GENERAL INFORMATION: APPLICANT: Anderson, Darrell R.	· <u></u>	
	Publicati		
	í		
	Db 438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475		
	QY 394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431		
LYS 437	Db 378 YTLPESRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS		
LYS 393	Qy 334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFI		

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TELEPHONE: 703-836-6620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-905-12
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US-10-124-905-12
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                                                                                           Query Match
Best Local S
Matches 274
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APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teakin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-13:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10762-6620
TELEPHONE: 703-036-6620
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APPLICANT: AND STREET: AND STREET: APPLICANT: AND STREET: APPLICANT: AND STREET: APPLICANT: AND STREET: APPLICANT: AND STREET: AND STREET: AND STREET: APPLICANT STREET: APPLICANT STREET: APPLICANT STREET: APPLICANT STREET: APPLICANT STREET: 699 Prince Street
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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MEDIUM TYPE: Floppy disk
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CITY: Alexandria
STATE: VA
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ZIP: 22314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS
                                                                                                                         Similarity
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                                                                                     52.7%; Score 1271; DB 13; llarity 59.8%; Pred. No. 2.3e-81; Conservative 29; Mismatches 87;
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                                                                                                                                              Length 476;
                                                                                           Indels
                                                                                           68;
                                                                                           Gaps
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US-10-124-807-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
FILING DATE:
CLASSIFICATION:
                              TELEPHONE: 703-836-662)
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,91
FILING DATE:
APPLICATION NUMBER: US 08/487
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STATE:
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ZIP: 22314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
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: VA
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No. US20030166207A1
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND
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US-10-291-532-12
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                                                                                                                                  NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10291532 Publication No. US20030180290A1 GENERAL INFORMATION:
                                                                                                                                                                                                                              TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REFERENCE: 037003/291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
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Best Local Similarity
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/487,950 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HARIHARAN, KANDASAMY APPLICANT: HANNA, NABIL
              ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: primatized peptide sequence
                                                                                               TYPE: PRT
                                                                                                                LENGTH: 476
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GY: linear
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Sequence 348, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 348
LENGTH: 504
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Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                              Matches 282;
                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                     1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---KNSN 57
                                        TVKLL----IYYT---SRLHSGVPSRFSGSGSGTDYSLTIANLQPEDIATYFCQ----- 112
                                                                          QIKILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203
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                                                                                                                   MSRGVDIQ-----MTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP
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                                                                                                                                                                                              29;
                                                                                                                                                                                            Score 1271; DB 14;
Pred. No. 2.5e-81;
29; Mismatches 92;
-----PGSSPSV 153
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Sequence 4278, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTMARE: PAtentin Ver. 2.1
SEQ ID NO 4278
LENGTH: 473
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-4278
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US-10-108-260A-4278
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                 248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
                                                         175 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP
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                                                                                                                                                                                                                                                                                                          VFLVALLRGVHCQGQLVQSGGGVVQPGRSLRLSCEASGFSFKFFNNHWVRQAPGKGLEWV
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                                                                                                                                                     ---KTLSVS-----TWTCTVLQNQKK 192
                                                                                                                                                                                   ----LVRGVHGAFD---LWGQGTLVTVSSASTKGPSVFFLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                                                               EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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유 상	dd Qy	Db Qy	Db Qy	Db Q	Db Oy	Qy ab	gb Qy	S-09- Quer Best Matc	CURRENT F. PRIOR APPI PRIOR FIL NUMBER OF SOFTWARE: SEQ ID NO LENGTH: TYPE: PRI ORGANISM FEATURE:	ESULT : Sequer Sequer Public GENERA APPLI APPLI APPLI TITLE FILE	Qy Db	Db Qy	рь рь
380 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431	20 TISKAKOOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOD 	FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 31	205 PEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 259	158 PRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPA 204	115KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRS 157	64 NQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQ 114	8 RHLLLVLQLALLPAATQGNKVVL-GKKGDTVELTCTASQKKSIQFHWKNSNQIKILG 63	600-32 tch 52.6%; Score 1270; DB 10; Length 6 al Similarity 57.8%; Pred. No. 3.7e-81; 273; Conservative 27; Mismatches 90; Indels	ILING DATE: 2001-07-20 LICATION NUMBER: 60/220,139 LING DATE: 2000-07-21 SEQ ID NOS: 32 Patentin Ver. 2.0 92 Patentin Ver. 2.0 93 12 13 15 16 19 17 18 18 28 29 20 20 20 21 21 22 22 23 24 25 26 26 27 28 28 28 28 28 28 28 28 28 28 28 28 28	SULT 52 -09-910-600-32 Sequence 32, Application US/09910600 Publication No. US20030036631A1 GENERAL INFORMATION: APPLICANT: Longphre, Malinda APPLICANT: Chang, Han APPLICANT: Whitney, Gena APPLICANT: Whitney, Gena TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF FILE REFERENCE: D0003NP CURRENT APPLICATION NUMBER: US/09/910.600	428 LSPG 431 469 LSPG 472	368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427 	308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367

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RESULT 54
US-10-656-769-20
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APPLICANT: Andras Aszodi
APPLICANT: Jose W. Saldanha
APPLICANT: Bruce M. Hall
ITITLE OF INVENTION: Therapeutic binding molecules
FILE REFERENCE: PCT/EP02/01420
CURRENT APPLICATION NUMBER: US/10/467,546
CURRENT FILING DATE: 2003-08-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
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US-10-467-546-4
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                                                                      Sequence 20, Application US/10656769 Publication No. US20040097712A1 GENERAL INFORMATION:
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Best Local Similarity 59.3
Conservative
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Publication No. US20040096901A1
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APPLICANT: Varnum, Brian
APPLICANT: Witte, Alison
APPLICANT: Vezina, Chris
APPLICANT: Wong, Lu Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gregorio Aversa
APPLICANT: Frank Kolbinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE OTHER INFORMATION: Amino acid sequence of chimeric heavy chain
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                                      SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                           SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-108-260A-4073
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US-10-108-260A-4073
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-20
                                                                                                                                                                                                                                                                                                                 APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOUTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4073
LENGTH: 472
TYPE OF THE ATTENTION TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOT
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TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
FILE REFERENCE: 01,1554
CURRENT APPLICATION NUMBER: US/10/656,769
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4073, Application US/10108260A Publication No. US20040005560A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 276; Conserv
                                                                           Matches
                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                   y Match 52.6%;
Local Similarity 59.5%;
hes 275; Conservative 24
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LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQ 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
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                                                                           24;
                                                                   Score 1269; DB 15;
Pred. No. 3.1e-81;
24; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81; Indels
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Sequence 4285, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
FILE REFERENCE: H1.A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4285
LENGTH: 471
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-4285
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US-10-108-260A-4285
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                                                                                                                                                                                                                                                                                       Query Match 52.5%; Score 1268.5; DB 15; Length 471; Best Local Similarity 57.2%; Pred. No. 3.4e-81; Matches 277; Conservative 37; Mismatches 85; Indels 85; Gaps
173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 195
                                                                                    167
                                                                                                                 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 PAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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                                                       YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP
                                                                                   ---KTLSVS------QLELQDSG------TWTCTVLQNQKK 192
                                                                                                               VVR-----GEDNYWGQGSLVIVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                         EWMGIRNP--SSGRSSVSQKFEGRLTLTADTSTTTAHMELRNLTSDDTGVYYCTTTRWKW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSF
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S	₽	γQ	B 4	ş	문 &	дg	Ş	Db	Ş	문	δ	₽	Ş	Query Best Match	Qy Qy Db RESULT 57 RESULT 57 US-10-416-(; Sequence ; Publicat: ; GENERAL ; APPLICAL ; APPLICAL ; APPLICAL ; APPLICAL ; APPLICAL ; TITLE OI ; FILE REI ; CURRENT ; CURRENT ; CURRENT ; CURRENT ; CURRENT ; CURRENT ; UMBER (CURRENT ; UMBER (CURRENT ; OTHER ; SOFTWAR ; SOFT	Db Qy	Db Qy
341 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 400	349 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 408	281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 340	GGPSVPLPPPKPKDTLM1SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ		176 LQDSGTWTCTVLQNQKKVEKLDIVPCPAPERKSCDKTHTCPELL 220	VSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQ	156LSVSQLE 175	115 TLPYTFGGGTKLEITGSTSGSGKP-GSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSG 173	114 QKESVDLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQC 155	62 PDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGN 114	55 NSNQIKILGNQGSFLTKG-PSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVED 113	2 LLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK 61	10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWK 54	Query Match 52.5%; Score 1268; DB 16; Length 634; Best Local Similarity 56.2%; Pred. No. 5.3e-81; Matches 287; Conservative 28; Mismatches 94; Indels 102; Gaps 16;	368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427	308 VSNKALPAPIEKTISKAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367 	248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307

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CURRENT APPLICATION NUMBER: US/10/226,435A
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/06191
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,601
PRIOR APPLICATION NUMBER: 60/254,465
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-12-08
PRIOR PRIOR PRIOR NUMBER: 60/254,498
PRIOR APPLICATION NUMBER: 60/254,498
PRIOR APPLICATION NUMBER: 60/254,498
PRIOR PRIOR DATE: 2000-12-08
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PRIOR PRIOR DATE: 2000-13-08
PRIOR PRIOR PRIOR DATE: 2000-13
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US-10-226-435A-12
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Publication No. US20040043418A1
GENERAL INFORMATION:
APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY
TITLE OF INVENTION: Humanized Antibodies that Sequester Amy
FILE REFERENCE: 8792/293
FILE REFERENCE: 8792/293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 274; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Humanized antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
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SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                     PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                            PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
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                                                                                                                                                                                                                                                EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                            THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --QLELQDSG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
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Sequence 2, Application US/10120198B
Publication No. US20030215427A1
; GENERAL INFORMATION:
APPLICANT: Jensen, Michael
TITLE OF INVENTION: CET-SPECIFIC REDIRECTED IMPLICANT APPLICATION NUMBER: US/10/120,198B
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/282,859
PRIOR APPLICATION NUMBER: 60/282,859
PRIOR PILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
TENGRUSE: 63
RESULT 60
US-09-925-179-68
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US-10-120-198B-2
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ORGANISM: artificial
FEATURE:
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nes 277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      SLQAEDFATYYCQQYWSTPFTFGSGTELEIKV-----EPKSSDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                                                                                                                                                           QLELQDSGTWTCT-----VLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELL 220
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                                                                                                     RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                          RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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; Pred. No. 6.8e-81;
39; Mismatches 84; I
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Sequence 68, Application US/09925179
Publication No. US20030044858A1
GEMERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-IGE Antibodies (as
FILE REFERENCE: P0718P2C1D1C1US

CURRENT APPLICATION NUMBER: US/09/925,179

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PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/082/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
LENGTH: 451
TYPE: PRT
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US-10-423-299-4
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                                                                                                                                                               Sequence 4, Application US/10423299
Publication No. US20030229212A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.4%;
Best Local Similarity 58.6%;
Matches 273; Conservative 29
APPLICANT: FAHRNER, ROBERT
APPLICANT: FOLLMAN, DEBORAH
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: LABRETON, BONDART
TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF
FILE REFERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/375,953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                               GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
                                                                                                                                                                                                                                                                                                                                                                      GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRDDSKNT-----FYLQLNSARAEDTAVYYCARGSH-----YFG------HWHFAV 110
                                                                                                                                                                                                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450
                                                                                                                                                                                                                                                                                                                       DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                          GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %; Score 1266; DB 10;
%; Pred. No. 4.8e-81;
25; Mismatches 78;
                                                                            PROTEINS
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APPLICANT: Simmons, Laura C.
APPLICANT: Kilmowski, Laura
APPLICANT: Kilmowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT APPLICATION NUMBER: US 60/256,164
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 9
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
COURSED INFORMATION: anti-TF heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Sequence is synthesized US-10-423-299-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 62
US-10-020-786-9
                                                       US-10-020-786-9
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10020786 Publication No. US20030073164A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 LGKKGDTVELTCTASQKKSIQFHWKN-----SNQIKILG--NQGSFLTKGPSKLNDR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------
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ilarity 58.9%;
Conservative 28
                                                                        anti-TF heavy chain
52.4%;
58.8%;
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Pred. No. 4.8e-81;
8; Mismatches 75
Score 1266; DB 14;
Pred. No. 5.1e-81;
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421

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CURRENT APPLICATION NUMBER: US/10/227,694
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US 60/315,209
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 470
TYPE: PRT
ORGANIEM: Artificial sequence
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US-10-227-694-5
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10227694
Publication No. US20030077739A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic -10-227-694-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Simmons, Laura
APPLICANT: Andersen, Dana
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
FILE REFERENCE: P1867R1
                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384
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                        128
                                                        134 -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                      DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
                                                                                           TISADNSKNTAYLOMN-----
                                                                                                                             ----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL--
                                                                                                                                                                LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA
                                                                                                                                                                                                    LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILG-NQGSFLTKGPSKLNDRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISADNSKNTAYLOMN-----SLRAEDTAVYYCA------RDTAAYF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILG-NQGSFLTKGPSKLNDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPK
                                                                                                                                                                                                                                    52.4%; Score 1266; DB 14; ilarity 58.8%; Pred. No. 5.1e-81; Conservative 26; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09848832
Publication No. US20030165507A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hooper, Douglas
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
TILE REFERENCE: HOO01.NP0002
CURRENT APPLICATION NUMBER: US/09/848,832
CURRENT APPLICATION NUMBER: 60/204,518
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 4
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nes 276; Conserv
325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                    GVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD-----KRVEPKS
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                                                                                                                                                                                                                                                                                                                                                                                  SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                                                                            DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
                                                                                                                                                 CDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
                                                                                                                                                                                                                                                                           YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 192
                                                                                                                                                                                                                                                                                                                                                                                                                       LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                             CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                          DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                         ----QLELQDSG-----
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APPLICANT: INCLEMENT OF INVENTION: Recombinant Antibodies, and TITLE OF INVENTION: Recombinant Antibodies, and TITLE OF INVENTION: And Methods for Making The FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-08-21
INUMBER OF SEQ ID NOS: 16
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 474
RESULT 66
US-10-461-148-1
; Sequence 1, Application US/10461148
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; ORGANISM: Homo sapiens
US-10-225-108A-3
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US-10-225-108A-3
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Best Local S
Matches 276
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Publication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
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276; Conservative
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                                                                                     SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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; Pred. No. 5.1e-81;
32; Mismatches 71;
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; Publication No. US20040013672A1
; GENERAL INFORMATION:
APPLICANT: Dietzschold, Bernhard
APPLICANT: Dietzschold, Bernhard
APPLICANT: Hooper, Douglas C.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT APPLICATION NUMBER: US 10/225,108
PRIOR APPLICATION NUMBER: US 10/225,108
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-16
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Sequence 240, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
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SEQ ID NO 1
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 LGKKGDTVELTCTAS------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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Pred. No. 5.1e-81;
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                                                                              FUSION
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Sequence 398, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069, 401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 398
LENGTH: 500
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
                                  ; OTHER INFORMATION: US-10-207-655-398
                                                                                                                                                                                                                                                                                                                                               RESULT 68
US-10-207-655-398
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SEQ ID NO 240
LENGTH: 500
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Best Local Similarity
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EWESNGQPENNYKTTPFVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAIYPGNGDTSYNOKFKGKATLTVDKSSSTAYMOLSSLTSEDSAVYFCARVVYYSNSYWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TANSDITHLLQ-GQSLITLILESPPGSSPSVQCR-----SPR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                     SLSLSPG
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52.4%;
Score 1266;
BB
14;
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Length 500;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Buyes, Marie-Ange
APPLICANT: Sablon, Erwin

TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC

TITLE OF INVENTION: SHOCK,

TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

FILE REFERENCE: INNS:015

CURRENT APPLICATION UNMBER: US/10/071,485

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737

PRIOR FILING DATE: 2000-02-14

PRIOR FILING DATE: 1998-08-14

PRIOR APPLICATION NUMBER: EPO 98/05165

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: EPO 98870139.7

PRIOR APPLICATION NUMBER: EPO 98870122.5

PRIOR APPLICATION NUMBER: EPO 97870122.5

PRIOR FILING DATE: 1997-08-18

NUMBER OF SEQ ID NOS: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 69
US-10-071-485-67
; Sequence 67, Application US/10071485
; Publication No. US20030099648A1
; Publication No. US20030099648A1
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                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 67
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                   Query Match
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                                                                                                         LENGTH: 468
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                   OTHER INFORMATION: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRSLWDQG-NFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGL------ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOGNKVVLGKKGDTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 56.3%; Pred. No. 5.5e-81; Conservative 27; Mismatches 94
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52.4%;
Score 1265.5; DB 14; Pred. No. 5.5e-81;
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                     Length 468;
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Best Local Similarity

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CURRENT APPLICATION NUMBER: US/10/071,485
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 09/485,737
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.0
SEQ ID NO 90
LENGTH: 711
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US-10-071-485-90
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                                                                             ; OTHER INFORMATION: US-10-071-485-90
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Query Match 52.4%; Score 1265.5; DB 14; Length 711; Best Local Similarity 57.2%; Pred. No. 9.2e-81; Matches 277; Conservative 31; Mismatches 79; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING
TITLE OF INVENTION: SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
                                                                                                                TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KTLSVS-----TWTCTVLQNQKK 192
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                                                                                                SYNTHETIC
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  13;
                                                                                                                                                                                                                                               APPLICANT: Sullivan, John
APPLICANT: Medlock, Eugene
APPLICANT: Medlock, Eugene
APPLICANT: Martin, Francis
TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: MBHB 01-1145-A
CURRENT FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42
LENGTH: 445
TYPE: PRT
ORGANT?
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US-10-408-901-42
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                                                                                                                                                     Query Match 52.4%; Score 1265; DB 16; Best Local Similarity 59.0%; Pred. No. 5.5e-81; Matches 271; Conservative 27; Mismatches 71;
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  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                                    SRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL 141
                                                                     GSIRLSCVGSRFTFSAYPMHWVRQAPGKGLEWVSGIGSGGGTNYADSVKGRFTIS-RDT
                                                                                                                GDTVELTCTASQ--KKSIQFHW-----KNSNQIKILGNQG----SFLTKGPSKLNDRAD
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AKNSLYLOMN-----SLRAEDMAVYYC---
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                                                                                                                                                 71;
----ARGRNSFDYWGQGTLV
                                                                                                                                                         Indels
                                                                                                                                                                                          Length 445;
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TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A
FILE REFERENCE: 040853-01-5082
CURRENT APPLICATION NUMBER: US(10/411,037)
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/387,797
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-28
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version
SEQ ID NO 56
                                                                                                                Matches
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Publication No.
                                                                                                                                                                                                      LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
-10-411-037-56
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                                                               KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRADSR
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                       KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR
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Bowe, Caryn
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                                                                                                                Conservative
                                                                                                           52.4%; Score 1265; DB 12; 58.7%; Pred. No. 5.6e-81; tive 26; Mismatches 80;
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                                                                                                                                                       Length 448;
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US-10-411-026-56
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                                                                                                                                                            US-10-411-026-56
                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 040853-01-5053
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/347,292
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                SEQ ID NO 56
                                                                                                           Query Match
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Publication No. US20040063911A1
                                                                   Matches
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS
                                                                                                                                                                                                    LENGTH: 44
TYPE: PRT
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                                                                                                                                                                            ORGANISM: Homo sapiens
                                                               y Match 52.4%; Score 1265; DB 12;
Local Similarity 58.7%; Pred. No. 5.6e-81;
hes 270; Conservative 26; Mismatches 80;
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32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRADSR 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
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Chen, Xi
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                                                                 Indels 84;
                                                                                                           Length
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Gaps

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RESULT 74
US-10-410-962-56
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                                                                                  ) ORGANISM: Homo US-10-410-962-56
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Query Match 52.4%; Score 1265; DB 16; Best Local Similarity 58.7%; Pred. No. 5.6e-81; Matches 270; Conservative 26; Mismatches 80;
                                                                                                                                           SEQ ID NO 56
LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR:
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REFERENCE: 040833-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
                                                                                                                                                                                 PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Neose Technologies,
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
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Zopf, David
Bayer, Robert
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Bowe, Caryn
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No. US20040077836A1
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US-10-411-049-56
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                                                                                SOFTWARE: PatentIn SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56, Application US/10411049 Publication No. US20040082026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
                                                                                                                                                          PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON TITLE OF INVENTION: ALPHA
FILE REFERENCE: 0400853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR PELICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
                                        LENGTH: 44
TYPE: PRT
                                                                                                                      NUMBER OF SEQ ID NOS: 75
                                                                                                                                         PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
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                  ORGANISM: Homo sapiens
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                                                             448
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Bayer, Robert
Hakes, David
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                                                                                                   version 3.2
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Gaps

67

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APPLICANT: Chen, X1

APPLICANT: Bowe, Caryn

TITLE OF INVENTION: BETA

FILE OF INVENTION: BETA

FILE OF INVENTION: BETA

FILE OF INVENTION: BETA

FILE REFERENCE: 040853-01-5056

CURRENT APPLICATION NUMBER: US/10/410,930

CURRENT APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR APPLICATION NUMBER: US 60/404,249
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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                                        SEQ ID NO 56
                                            NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3 2
EQ ID NO 56
                                                                                                         PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                    LENGTH:
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Pred. No. 5.6e-81;
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US-10-410-997-56
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               PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                              FILE REFERENCE: 040853-01-5059
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
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APPLICANT: Defrees, Shawn
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PatentIn version 3.2
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Bowe, Caryn
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Hakes, David
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Pred. No. 5.6e-81;
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; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-56
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Publication No. US20040132640A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, David
APPLICANT: Zopf, David
APPLICANT: Hakes, David
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US-10-411-012-56
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PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/347,292
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR PILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/407,527
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                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GLYCOPEGYLATION METHODS TITLE OF INVENTION: METHODS FILE REFERENCE: 040853-01-5051 CURRENT APPLICATION NUMBER: US/10/411,012 CURRENT FILING DATE: 2003-04-09
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
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NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
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TYPE: PRT
ORGANISM: Homo sapiens
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                 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                       ELODSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC
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                                                                             QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                       AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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                                                           QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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ilarity 58.7%;
Conservative 26
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Pred. No. 5.6e-81
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RESULT 79

US-10-287-994-56

Sequence 56, Application US/10287994

Publication No. US20040137557A1

GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: Zopf, David

APPLICANT: Zopf, David

APPLICANT: Bayer, Robert

APPLICANT: Bowe, Caryn

APPLICANT: Chen, Xi

TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES

FILE REFERENCE: 040853-01-5052-00

CURRENT APPLICATION NUMBER: US/10/287,994

CURRENT FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR APPLICATION NUMBER: US 60/396,594

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PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PACENTIN VERSION 3.1
SEQ ID NO 56
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-994-56
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US-10-410-913-56
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Publication No. US20040142856A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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             PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
                                                                                                                                          FILE REFERENCE: 040853-01-5081
CURRENT APPLICATION NUMBER: US/10/410,913
CURRENT FILING DATE: 2003-04-09
                                                                                                                                                                                             APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GLYCOCONJUGATION METHODS
TITLE OF INVENTION: METHODS
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FILING DATE:
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                                                                                                                                                                                                                                                                  Bayer, Robert
Hakes, David
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PRIOR FILING DATE: 2002-07-17
PRIOR PPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
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ORGANISM: Homo sapiens
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                     392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC
                                                                                             QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
                                                                                                                                                  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                                            PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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                                                                        QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                                                                       AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Pred. No. 5.6e-81;
6; Mismatches 80;
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RESULT 81
US-09-773-877A-18
US-09-773-877A-18
Sequence 18, Application US/09773877A
Publication No. US20030017977A1
ITITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 462
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fit1(2-3)-Fc (Mut3)
US-09-773-877A-18
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Query Match

Best Local Similarity

52.4**%**; 65.7**%**;

Score 1265; DB 12; Pred. No. 5.8e-81;

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RESULT 82
US-09-773-877A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-773-877A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09773877A

Publication No. US20030017977A1

GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT ETLING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0

SEQ ID NO 12
LENGTH: 567
TYPE: PRT
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Best Local Similarity
Matches 255; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Flt(1-3)-Fc
                          284
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TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                  PVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTI 298
                                                                                                                                                                                                                                                                                                                     DGKRIIWDSRK-GFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPR 238
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                                                                 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                       SVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 283
                                                                                                                                                     DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP
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; Pred. No. 7.5e-81;
24; Mismatches 71;
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US-09-875-338-9
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LENGTH: 698
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APPLICANT: ZHOU, XIA-DI
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
TITLE OF INVENTION: INVUNOMODULATION
FILE REFERENCE: 3053-4071US2
CURRENT APPLICATION NUMBER: US/09/875,338
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver: 2.1
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APPLICANT:
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                                                                                              QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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FINGER, JOSHUA N.
YANG, GUCHEN
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RESULT 85
US-09-773-877A-20
; Sequence 20, Application US/09773877A
; Publication No. US20030017977A1
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US-10-077-023-9
¡Sequence 9, Application US/10077023
; Publication No. US20030031675A1
; GENERAL INFORMATION:
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GENERAL INFORMATION:
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APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL
TITLE OF INVENTION: IMMUNOMODULATION
FILE REFERENCE: 3053-4071US3
CURRENT APPLICATION NUMBER: US/10/077,023
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/272,107
PRIOR PILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
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APPLICANT: CHANG, HAN
APPLICANT: FINGER, JOS
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PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 138
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ORGANISM: Artificial Sequence
FEATURE:
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67.8%; Pred. No. 9.8e-81;
tive 18; Mismatches 57
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GENERAL INFORMATION:
APPLICANT: Young, Jame
APPLICANT: Johnson, I
APPLICANT: Huse, Will
APPLICANT: Wu, Herrer
APPLICANT: Watkins, J
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US-09-796-848A-37
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                                                                                                 APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods
TITLE OF INVENTION: Producing Them
FILE REFERENCE: 469201-526
CURRENT FILIG DATE: 2001-10-30
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 567
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Patent No. US20020098189A1
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Best Local Similarity 65.7
Matches 255; Conservative
                                                             LENGTH: 45
TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain
                                        ORGANISM: Artificial Sequence
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                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 DTHLLQGQSLTL--TLESPPGSSPSVQCRSPRGKNIQGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                                                  Huse, William D.
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                                                                                                                                                                                                                                                                                                                                                  Wu, Herren
                                                                                                                                                                                                                                                                                                                                                                                             , James F.
son, Leslie
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RESULT 87

US-09-796-848A-45

Sequence 45, Application US/09796848A

Patent No. US20020098189A1

GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wuk, Herren
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: High Potency Recombinant Ant
FILE REFERENCE: 469201-526
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/796,848A
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 450
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: high potency antibody. US-09-796-848A-45
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Best Local Similarity 57.8
Matches 271; Conservative
                                  Query Match
Best Local Similarity
Matches 271; Conserv
                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL-----NDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVKPTQTLTLTCTFS-----GFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSRRSLWD-----QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT
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                                  52.3%; Score 1263.5; DB 9; ilarity 57.8%; Pred. No. 7.2e-81; Conservative 27; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.3%; Score 1263.5; DB 9; 57.8%; Pred. No. 7.2e-81; tive 27; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies and Methods
                                                                  DB 9;
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US-09-996-288-220
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
TITLE OF INVENTION: and Treatment
FILE REPERENCE: 10271-047-999
CURRENT APPLICATION UNMEER: US/99/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 220
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 220, Application US/09996288 Patent No. US20020177126A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                   173 -----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
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                                                                                                                                                                                                                                                                                                       271;
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                                                                                                                                                                                                                                                     30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL------NDRA
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                                                                                                HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS----- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59
                                                                                                                                                   DYNPSIKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD-----MIFNFYFD--- 108
                                                                                                                                                                                                                          LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSRRSLWD------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
                                                                                                                                                                                     DSRRSLWD------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
                                                                        -- VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                   52.3%; Score 1263,5;
57.8%; Pred. No. 7.20
tive 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                        DB 9;
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APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 226
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-996-288-226
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Best Local
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                       LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                         YVDGVEVHNAKTKPREEQYNGTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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57.8%;
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Pred. No. 7.2e-81;
27; Mismatches 74
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; Sequence 234, Application
; Patent No. US20020177126A1
; GENERAL INFORMATION:
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APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
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US-09-996-288-232
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US-09-996-288-232
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Patent No. US2002017126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION UNDERS: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOOTWARE: PatentIn version 3.1
SEQ ID NO 232
LENGTH: 450
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ORGANISM: Homo
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                            LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                   KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
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                                                                                                                                                                                  YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                      KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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US/09996288

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; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3
; SEQ ID NO 234
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Bapiens
US-09-996-288-234
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US-09-996-288-236
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APPLICANT: Voung, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/9/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 236
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-236
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Patent No. US20020177126A1
GENERAL INFORMATION:
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Best Local Similarity 57.8
Matches 271; Conservative
                                                                    Query Match 52.3%; Score 1263.5; DB 9; Length Best Local Similarity 57.8%; Pred. No. 7.2e-81; Matches 271; Conservative 27; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVKPTQTLTLTCTFS-------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK
     LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59
                                    LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL------NDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.3%; Score 1263.5; DB 9; 57.8%; Pred. No. 7.2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Mismatches
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APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTMARE: Patentin version 3.1
SEQ ID NO 238
LENGTH: 450
TWORE: DOSE
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US-09-996-288-238
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Best Local Similarity 57.8%;
Matches 271; Conservative 26
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KSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                         -- VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
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                                                                                                                                                                                            DYNPSIKSRITISKDTSKNQVVIKVTNMDPADTATYYC----ARDMITNFYFD-----
                                                                                                                                                                                                                               DSRRSL-----WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                                                                                                                                                                                                                                                                 LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK
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KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                                                                                       -----QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEP
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                                                                                                                                                                                                                                                                                                                                    Score 1263.5; DB 9;
Pred. No. 7.2e-81;
6; Mismatches 75;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 242
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-242
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US-09-996-288-242
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Patent No. US2002
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Best Local Similarity
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                                                             KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
                                                                                                                                                                                          KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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20020177126A1
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57.8%; Pred. No. 7.26
tive 26; Mismatches
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75;
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RESULT 96
US-09-996-288-246
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APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi:
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 244
Sequence 246, Application US/09996288 Patent No. US20020177126A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                            LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Pred. No. 7.2e-81;
6; Mismatches 75;
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APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259

Anti-RSV Antibodies for Prophylaxi

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; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-996-288-246
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                                                                                                                                                                                                     Sequence 252, Application US/09996288
Patent No. US2002017126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Lesie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION UNMER: US/99/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOCTWARE: PatentIn version 3.1
SEQ ID NO 252
LENGTH: 450
TYPE: PRT
                                                                                            Query Match 52.3%; Score 1263.5; DB 9; Length Best Local Similarity 57.8%; Pred. No. 7.2e-81; Matches 271; Conservative 27; Mismatches 74; Indels
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DSRRSLWD-----QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
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                KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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Sequence 254, Application US/09996288 Patent No. US20020177126A1 GENERAL INFORMATION:
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APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
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TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax1
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant Query Match 52.3%; Score 1263.5; DB 9; Length Best Local Similarity 57.8%; Pred. No. 7.2e-81; Matches 271; Conservative 27; Mismatches 74; Indels 132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL------NDRA 80 81 DSRRSLWD------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131 HYNPSLKDRITISKDTSKNQVVLKVTNMDPADTATYYCARD-----MIFNFYFD-----VMGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGAL KSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW -----GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 97; Gaps 262 166 59 11

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APPLICANT: Voung, James
APPLICANT: Scott, Koenig
APPLICANT: Leglie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/99/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOCTWARE: Patentin version 3.1
SEQ ID NO 256
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-256
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                  LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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GENERAL INFORMATION:

APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
FILE REFERENCE: 10271-048-999
CURRENT APPLICATION NUMBER: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SEQ ID NO 220
LENGTH: 450
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD-----MIFNFYFD---
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                                                                                              KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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US-09-485-737B-90
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US-09-248-737B-71
US-09-248-737B-71
US-09-228-246-625-3
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US-09-234-347A-71
US-09-234-347A-71
US-09-234-347A-71
US-09-234-347A-71
US-09-236-0145-2
US-09-249-846-1131-8
US-09-249-846-128-18
US-09-249-846-128-18
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CORRESPONDENCE ADUNESS:
ADDRESSEE: COOPET & Dunham
STREET: 30 ROCKefeller Plaza
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9809
TELEFAX: (212) 977-9809
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
I.RNGTH: 432 amino acids
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US-08-477-460B-2
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOC
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
               LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
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US-09-761-413-2
US-08-784-512-3
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US-09-176-288-3
US-09-173-656-1
US-09-227-595-24
US-08-227-595-24
US-08-227-595-24
US-08-227-656-16
US-09-131-247-16
US-09-131-247-16
US-09-131-247-16
US-09-131-247-14
US-09-131-247-14
US-09-131-247-14
US-09-131-247-14
US-09-746-359A-62
US-09-487-659A-23
US-09-4470-299-4
US-09-4470-299-4
US-09-4480-359A-63
US-09-446-359A-63
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; ORGANISM: hom
; CELL TYPE: ly:
US-08-477-460B-2
                                                                  Query Match
Best Local S
Matches 405
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Patent No. 6083478
GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: Inmunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER APPLICATION NUMBER: 07/927,931
EARLIER FILING DATE: 1992-08-07
EARLIER FILING DATE: 1992-08-07
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Best Local Similarity 91.2
Matches 405; Conservative
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SOFTWARE: PatentIn Ver
SEQ ID NO 2
LENGTH: 432
                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                  Score 2122; DB 3;
Pred. No. 3e-164;
8; Mismatches 5;
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Pred. No. 3e-164;
8; Mismatches 5;
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PRIOR APPLICATION NUMBER: 08/477,460

RILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEPHONE: (212) 977-9809

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09329916
Patent No. 6177549
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Progenics Pho
TITLE OF INVENTION: NON-
TITLE OF INVENTION: CD4
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPONITION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/477,460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 30 Rockefeller Plaza CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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NON-PEPTIDYL MOIETY-CONJUGATED
CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                US/09/329,916
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; ORIGINAL SOURCE:
; ORGANISM: homo
; CELL TYPE: lym
US-09-329-916-2
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08485372A
Patent No. 6187748
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4
NUMBER OF SEQUENCES: 9
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US-08-485-372A-2
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Best Local S
Matches 405
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/476,227
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & D
STREET: 1185 Avenue o
CITY: New York
STATE: New York
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036
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405; Conservative
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1185 Avenue of the
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91.2%;
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Pred. No. 3e-164;
8; Mismatches
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RESULT 3 US-09-329-916-2

COUNTRY: U

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RESULT 5
US-09-409-006A-2
US-09-409-006A-2
; Sequence 2, Application US/09409006A
; Patent No. 6342586
; Patent No. 6342586
; GENERAL INFORMATION:
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CELL TYPE: lymphocyte
US-08-485-372A-2
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Best Local Similarity 91.3
Matches 405; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                 APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: MON-PEPTITYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPET & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
     COMPUTER READABLE FORM:
                   COUNTRY: U
                                                   CITY: New York
STATE: New York
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STRANDEDNESS: unl
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91.2%;
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Pred. No. 3e-164;
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US-08-484-681-2

IS-08-484-681-2

; Sequence 2, Application US/08484681

; Patent No. 6451313

; GENERAL INFORMATION:
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TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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Best Local
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
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APPLICATION NUMBER: US 07/927
RILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION:
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ORIGINAL SOURCE:
ORGANISM: hom
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STRANDEDNESS: unl
TOPOLOGY: unknown
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                                                                                                                                                                                                         VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
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                                                                                                                                     FSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                         FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
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                                                                                                                                                                                     VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                                                                                                                                                       VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
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                                                                                                                     FSCSVMHEALHNHYTQKSLSLSPG
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91.2%;
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Pred. No. 3e-164;
9. Mismatches 5;
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US-08-484-681-2
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Best Local S
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York

STATE: New York
COUNTRY: 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 37/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TYPE: amino acid
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                                                          VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                                      VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
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FSCSVMHEALHNHYTQKSLSLSPG 431
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                                    VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
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lymphocyte
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Maddon, Paul
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Pred. No. 3e-164;
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PCT-US93-07422-2
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APPLICATION NUMBER: US 07/927,
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 977-9809
TELEPAX: (212) 977-9809
TELEY: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceutic
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Best Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:
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FILING DATE: 19930800
CLASSIFICATION:
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
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CORRESPONDENCE ADDRESS:
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CELL TYPE:
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TOPOLOGY: unk
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| FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
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                                                         TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP-
                                                                                           TWTCTVLQNQKKVEFKIDIV-------PCPAPEPKSCDKTHTCPELLGGPSVFL
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91.2%;
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Pred. No. 3e-164;
8; Mismatches
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Query Match 86.7%; Score 2092; DB 4; Length 630; Best Local Similarity 67.2%; Pred. No. 1.4e-161; Matches 424; Conservative 0; Mismatches 5; Indels 202; Gaps 5; Qy 1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60	TELEPHONE: 617-428-7045 TELEPAX: 617-428-7045 TELEX: INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 630 amino acids TYPE: amino acids STRANDEDNESS: unknown TOPOLOGY: linear MOLECULE TYPE: protein US-08-472-888A-6	SOFTWARE: FABISEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/472,888A FILING DATE: 07-JUN-1995 CLASSIFICATION 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/618,314 FILING DATE: 23-NOV-1990 ATTORNEY/AGENT INFORMATION: NAME: Elbing, Karen L REGISTRATION NUMBER: 35,238 REFERENCE/DOCKET NUMBER: 00786/258001		ESULT S-08 S-que Seque Pater GENI AI TT	Db 228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287 Qy 288 VSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
PRIOR APPLICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/927,931 FILING DATE: 07-AUG-1992 ATTORNEY/AGENT IMFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM TELECOMUNICATION INFORMATION: TELEPHONE: (212) 977-9850 TELEPAX: (212) 977-9809 TELEX: 422523 COOP UI	CITY: New York COUNTRY: USA COUNTRY: USA COUNTRY: USA ZIP: 10112 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/477,460B FILING DATE: 07-JUN-1995	# H H L O O D F	Qy 341 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 400	QY 201PC	

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Sequence 4, Application US/08379516

Patent No. 6083478

GENERAL INFORMATION:

APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-

TITLE OF INVENTION: Immunoconjugatee and Uses Thereof

FILE REFERENCE: 41215-A-PCT-US

CURRENT APPLICATION NUMBER: US/08/379,516

CURRENT FILING DATE: 1995-06-10

EARLIER APPLICATION NUMBER: PCT/US93/07422

EARLIER FILING DATE: 1993-08-06

EARLIER APPLICATION NUMBER: 07/927,931

EARLIER PILING DATE: 1993-08-07

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4
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US-08-379-516-4
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Best Local Simi
Matches 409;
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Pred. No. 4e-161;
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US-08-379-516-4
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ORGANISM:
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                     LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE:
APPLICATION USA
ZIP: 10112
COMPUTER READABLE FORM:
APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE: 01-1014
APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995

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US-08-485-372A-4
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9809
TELEFAX: (212) 977-9809
TELEFX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 antino acids
                                                                                       Sequence 4, Application US/08485372A Patent No. 6187748 GENERAL INFORMATION:
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                 APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
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ORIGINAL SOURCE:
ORGANISM: homo sar
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ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-I
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: ORIGINAL SOURCE:
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COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
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LENGTH: 530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: unl TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homo sapien CELL TYPE: lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 278-04
TELEPAX: (212) 391-0525
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
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                 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                   TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW
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KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM
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APPLICATION NUMBER: US 07/927,931

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-950

TELEPHONE: (212) 977-9809

TELEEX: 422532 COOP UI

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 amino acids
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US-09-409-006A-4
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                 Local Similarity
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FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                             121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                      TWTCTVLQNQKKVEFKIDIV------PEP
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Pred. No. 4e-161;
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9; Mis
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                                                                  ; CELL TYPE:
US-08-484-681-4
 Best Loc
Matches
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                               Query Match
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John p.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beaudry, APPLICANT: Maddon, PITITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                 LENGTH: 530 amino TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.2
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               Local
                                                                                                    ORGANISM:
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                      TELEFAX: (212) 391-0525
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             Similarity
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1185 Avenue of the Americas
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 86.4%;
ilarity 77.3%;
Conservative
                                                                                                                                                   unknown
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lymphocyte
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Score 2085; DB 4;
Pred. No. 4e-161;
9; Mismatches 13;
                               Length 530;
 Indels
 98;
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 Gaps
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RESULT 15
PCT-US93-07422-4
                                FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
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GENERAL INFORMATION:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
APPLICATION NUMBER: US 07/927,931
FILTMG DATE: 07-ANG-1992
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 30 STREET: New York
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N
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                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08630172 Patent No. 6060054
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 409; Conserv
               ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
                                                                                                                                                                                                                   APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                               STREET: 1700 I
CITY: Denver
STATE: Colorac
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APPLICATION NUMBER:
                                                                                                                                            COUNTRY:
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Pred. No. 4e-161;
9; Mismatches 1
                                    Version
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09375419 Patent No. 6264950
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Best Local Similarity
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             APPLICANT: Staerz, Uwe TITLE OF INVENTION: NOT TITLE OF INVENTION: LYI
                                                                                                                                                                                       NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
                                                                                                                                     STREET: 1700 Linc
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDAGTWICTVLQNQKKVEFKIDIVVLAEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.2%;
                                                                                                                                                                                                                                                                    NOVEL PRODUCT AND PROCESS FOR T LYMPHOCYTE VETO
US/09/375,419
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Best Local Similarity 75.8%; Pr
Conservative 31;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 410 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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   353
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                      NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                             APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
                                                                                                                                                                                                                                     -----PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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NYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 409
                                                                                                                                                                              DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                   RGPTIKPCP---PCKC----PAPNILGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSED
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                                                                         APIERTISKPKGSVRAPQVYVLPPP-EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTEL
                                                                                                                                             DPDVQISWFVNNVEVHTAQTQTHREDYNSRLRVVSALPIQHQDWMSGKEFKCKVNNKDLP
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Pred. No. 9.4e-126;
1; Mismatches 51;
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US-08-284-391B-33

US-08-284-391B-33

Sequence 33, Application US/08284391B

Patent No. 5851828

Patent No. 5851828

GENERAL INFORMATION:

APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Banapour, Babak
APPLICANT: Kolanus, Waldemar

TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED

TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS

CORRESPONDENCE ADDRESS:

ADDRESSEB: Clark & Elbing LLP
STREET: 176 Federal Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
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RESULT 19
US-09-218-950-33
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                                                                                                                                                                                                  Sequence 33, Patent No. 6
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Best Local Similarity 98.0%;
Matches 249; Conservative
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Seed, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 0
FILING DATE: 14-FEB-11
APPLICATION NUMBER: 0
                                                   APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEJ
NUMBER OF SEQUENCES: 53
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1i
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Boston
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IMBER: 07/847,566
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; Sequence 7, Application US/08157101A
Patent No. 5808032
; GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
                                                                                                                                                                                                                                                                                                    RESULT 20
US-08-157-101A-7
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Best Local Similarity
Matches 249; Conserv
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APPLICATION NUMBER: US/08/284,39:

FILING DATE: 02-AUG-1994

APPLICATION NUMBER: 08/195,395

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 06-MAR-1992

APPLICATION NUMBER: 07/665,961

FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Blbing, Karen L

REGISTRATION NUMBER: 35,238

REGISTRATION NUMBER: 35,238
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LENGTH: 254 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWADD: The state of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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Pred. No. 6e-101;
0; Mismatches 0;
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NAME: TITUS, WARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEPAX: 202-861-3711
TELEPAX: 202-862-094
TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 enino acids
TYDE: Enicocid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.2%; Score 1284.5; DB Best Local Similarity 59.4%; Pred. No. 3.3e-96. Matches 280; Conservative 30; Mismatches 68
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PLA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
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                   PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSSPG 431
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                                                                                              ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 458
                                                                        ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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1100 NEW YORK AVENUE, N.W.
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US-08-397-411-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.1%; Score 1282.5; DB 3; Best Local Similarity 59.8%; Pred. No. 4.6e-96; Matches 274; Conservative 25; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Applic Patent No. 6129914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
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TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                               CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                         ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                        QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                                                                                                                                                                                                                    VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
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                                                                                                                                                                             QDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
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APPLICANT: MORROW, PHILLIP
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 475
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US-09-740-002-25
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ORGANISM: Homo sapiens
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HYTQKSLSLSPG 431
                                     SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                         SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                               NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                       NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                        RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQEWL
                                                                                                                                                                                                                  RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
                                                                                                                                                                                                                                                                    NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
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US-07-934-373C-22
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-UN-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
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APPLICANT: Paul J. Car
APPLICANT: Leonard G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: A
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650/225-1994
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                                                                                                                                                                                                                                                                                                                                    30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTK-GPSKLNDRADSRRSL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H: 454 amino acids
Amino Acid
                                                                                                                                                                                TLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QLE 175
PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                   ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                                                                LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD
                                                                                                                                                                                                                                                            ---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ---GQSLTL 141
                                                                                                                                                                                                                                                                                               LVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSHNQRFMDKATL
                                                                                                                                               TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
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US-08-437-642B-22
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GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 454 mino acids
                                                                                                                      Query Match
Best Local Similarity
Matches 275; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-Msy-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
ETI.TNC DATE: 17-NOV-1943
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                                                                                                                                                                                                         TYPE: Amino acids
TYPE: Amino Acid
TOPOLOGY: Line-
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/71527
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
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STREET: 1 ....
CITY: South San Fre
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEPAX: 650/952-9881
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---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
                                        LVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSHNQRFMDKATL
                                                                              LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTK-GPSKLNDRADSRRSL
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1 DNA Way
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                                                                                                                  52.8%; Score 1274.5; DB 3; Length 454; 59.9%; Pred. No. 2.1e-95; ative 24; Mismatches 87; Indels 73;
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                                                                                                                    Gaps
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US-08-146-206C-22
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                                                                            US-08-146-206C-22
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Query Match 52.8%; So Best Local Similarity 59.9%; Pr Matches 275; Conservative 24;
                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
                                                                                                                                                                         TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
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CORRESPONDENCE ADDRESS
                                                                                                          TYPE: Amino Acid
                                                                                            TOPOLOGY:
                                                                                                                                                                                                             TELEPHONE:
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-- San Francisco
                                                                                              Linear
                                                                                                                                                                                                               650/225-1994
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Score 1274.5; DB 4;
Pred. No. 2.1e-95;
!4; Mismatches 87;
                                                                                                                                                                                                                                                       P0709P1
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  Indels
                                  Length 454;
  73;
Gaps
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RESULT 26
US-09-705-686-22
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Patent No. 6639055
GENERAL INFORMATION:
INFORMATION FOR
                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb flop;

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Windatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705,686

FILING DATE: 02-No. 6639055-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
                                APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P:
TELEPHONE: 650/225-1994
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presta, Leonard
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carter, Paul J.
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STATE: California
COUNTRY: USA
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                TELEFAX: 650/952-9881
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SEQ ID NO:
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; TOPOLOGY: Linear ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-705-686-22
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PCT-US93-07832-22
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application I
GENERAL INFORMATION:
APPLICANT: Genentech,
TITLE OF INVENTION: I
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Best Local Similarity
Matches 275; Conserv
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb fl.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US93/0783
FILING DATE: 1930820
CLASSIFICATION UNMBER: 07/715272
APPLICATION NUMBER: 07/715272
APPLICATION NUMBER: 07/715272
APPLICATION NUMBER: 07/715272
              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                       STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
FILING DATE:
                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
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                                                                                                                                                                                                                                                                           USA
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15-JUN-1992
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                 PCT/US92/05126
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                                                                                                                                      PCT/US93/07832
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                                                                                                                                                                                                                      360 Kb floppy disk
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                                                                                                                                                                                                                                                                                                                           Blvd
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PRIOR APPLICATION DATA:

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US-09-049-672A-4
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                             GENERAL INFORMATION:

APPLICANT: Hilman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Bughn, Mariah R.

TITLE OF INVENTION: HUMAN IMMUNE SY

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Travera
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INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                               Sequence 4,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 275; Conserv
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  STREET:
             ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTK-GPSKLNDRADSRRSL
                                                                                                                                                                                                                  , Application US/09049672A 6135941
                                                                                                                                                                                                                                                                                                                                                                                                              KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                        VTTLPESREEMIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLESPPGSSPSVOCRSPRGKNIQGG-----KTLSVS-----QLE
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                                                                                                                                                                                                                                                                                                    SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 453
                                                                                                                                                                                                                                                                                                                           SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                     VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSHNQRFMDKATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---WDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL
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                                                                     SYSTEM ASSOCIATED PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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              LSLSPG 431
LSLSPG
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Query Match 52.8%;
Best Local Similarity 57.2%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: PANCTU
CLONE: 1513264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 KILGNO--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                       CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
                                                                                                                                                                                                                                                                                PGKGLEWIGYIYYSGSTLYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDD-
                          WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                          KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NH
                                                                                                                                                                                                                                                                                                                                                                                                                        ----KTLSVS------QLELQDSG-----TWTCTVLQNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VGLRGGNYGMDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV 172
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                              CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                         CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
                                                                                                                                                                                                                                                                                                             KKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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Pred. No. 2.26
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286 245 230

346

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466

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Sequence 27, Application US/09740002

Patent No. 6537809

GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
APPLICANT: HORROW, PHILLIP
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CCURRENT APPLICATION NUMBER: US/09/740,002
CCURRENT FILING DATE: 1090-06-10
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-19
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
150CTH. 475
TRESULT 30
US-09-499-846-6
; Sequence 6, Application US/09499846
; Patent No. 6656728
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; ORGANISM: Homo sapiens
US-09-740-002-27
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US-09-740-002-27
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                                                                                                                                      SPG 431
                                                                                                                                                                      NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                           NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                             SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                                                                         NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                                                                                                     EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                       FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KTLSVS-----TWTCTVLQNQKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSFYLF-----YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 177
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                                                                                                                                                                                                                                         SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                      474
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GENERAL INFORMATION:

30;

91;

Gaps

12;

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GENERAL INFORMATION:
APPLICANT: KAVANAUSH et al.
APPLICANT: KAVANAUSH et al.
TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU.
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 525
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TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU:
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
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; ORGANISM: Homo
US-09-499-846-6
                                                                          US-09-499-846-4
                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
US-09-499-846-4
Query Match
Best Local Similarity
Matches 276; Conserv
                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09499846 Patent No. 6656728
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                                                                                         TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 276; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWSIIMDSVVPS---
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52.8%; ilarity 57.5%; Conservative 3
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57.5%;
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Score 1273.5; DB 4;
Pred. No. 3.1e-95;
0; Mismatches 83;
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                                  Length
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Sequence 2, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: KAVANAUGH et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
; FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTMARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-499-846-2
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US-09-499-846-2
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Best Local Similarity
Matches 276; Conserv
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                                                                                                         124 GLTANSDTHLLQGQSLTLTLESPP------GSS------PSVQCRSPRGKNI- 163
                                                                                                                                          207 -----RYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQA
                                                                                                                                                                                                                 162 KLHAVPAA------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKV---
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DKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLESRG
                                  -QGGKTLSVSQLELQDSGTWTC------TVLQNQKK------VEFKI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
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                                                                     GLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                     52.8%; Score 1273.5; DB 4; Length 622;
57.0%; Pred. No. 3.9e-95;
ative 31; Mismatches 86; Indels 91;
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APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FRP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER FILING DATE: 1998-04-30
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
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US-09-301-593-18
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Patent No. 6455677
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          Match 52.7%; Score 1271.5; DB 4; Length Local Similarity 59.0%; Pred. No. 3.7e-95;
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                                 PCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNA
                                                                                                     LQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-
                                                                                                                                                                                                                                                                                  W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
                                                                                                                                                                                                                                                                                                                 GLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                     ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                            TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179
                                                                                                                                                                                                               TLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----QLE
                                                                                                                                                                                                                                                TVGKSSSTAYMELRSLTSEDSAVYFC-----ARRRIAYGY---DEGHAMDYWGQGTSV
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                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPACTIBLE
COMPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION UMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION UMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ ID NO: 12:
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US-08-487-550-12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Matches 274;
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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CORRESPONDENCE ADDRESS
ADDRESSEE: BURNS, DO
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                                  177
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                                    QDSG----
                                                                   VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                     LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS---
                                                                                                                                                                         L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                                                                                                                                                                                                           LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
                                                                                                                                                                                                                                          LGKKGDTVELTCTASQ----KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS
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                                                                                                                                        ISTDTSKNOFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY----NNWFDVWGPGVLVT
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND
IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                               52.7%; Score 1271; DB 3;
59.8%; Pred. No. 4.3e-95;
tive 29; Mismatches 87
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                                                                                                                                                                                                                                                                             29;
                                  ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                              Length 476;
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USE THEREOF
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257
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US-09-526-098-12
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APPLICANT: Anderson,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                      Query Match
Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12,
                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US OF
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: V
                                                                                                                                                                                                                                                                                                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                  LGKKGDTVELTCTASQ----KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
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                                                                                                                                                              protein
                                                                    52.7%; Score 1271; DB 4; 59.8%; Pred. No. 4.3e-95; tive 29; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Street
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USE THEREOF
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CURRENT APPLICATION UNMEER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION UNMEER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION UNMBER: EPO 98870139.7
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1998-08-19
PRIOR PRIOR DATE: 1998-08-19
PRIOR PRIOR DATE: 1998-08-19
PRIOR DATE: 1998-08-19
PRIOR DATE: 1998-08-19
PRIOR DATE: 19
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US-09-485-737B-67
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PATENT NO. 6350860
GENERRAL INFORMATION:
APPLICANT: Buyee, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438
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                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                      17 VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L
                                                                                                                                                                                                                                                                                                                                11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
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                                                                                   QLLVFGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                                                                                                                                          KGPSKLNDRADSRRSLWD-QGNFP-----LIIKNLKIEDSDTYICEVEDQKEEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
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                                                                                                                                                KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC------
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                                                                                                                                                                                                                                                                                                                                                                                          52.4%; Score 1265.5; DB 4; Length 468; ilarity 57.2%; Pred. No. 1.2e-94; Conservative 31; Mismatches 79; Indels 97;
                         ----ARRGFYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
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APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERRERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: ECT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENTALE PATENT NOWER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENT NOWER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENT NOWER: EPO 97870122.5
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US-09-485-737B-90
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70
YFPEPVTVŚWNSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP
                                                                                                                                                                                                                                                                                                                                                                                       VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGNNWVKQAPGQG---L 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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                                                                                   ---KTLSVS-----TWTCTVLQNQKK 192
                                                                                                                                                                             KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPG 431
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                                                                                                                                                ----ARRGFYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%; Score 1265.5; DB 4; 57.2%; Pred. No. 2.1e-94; tive 31; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 711;
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US-08-458-516-13
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                                                                                                                                                                                                   US-08-458-516-13
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
EILING DATE: 03-MAX-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
REFERENCE/DOCKET NUMBER: 11823-37-3
REFERENCE/IDOCKET NUMBER: 11823-37-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08458516 Patent No. 5777085
                                                                                                 Matches 270;
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CLASSIFICATION: 424
                                                                                                                         Local Similarity
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KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR
                                              KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG----SFLTKGPSKLNDRADSR
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                                                                                            52.4%; Score 1265; DB 1;
58.7%; Pred. No. 1.2e-94;
ative 26; Mismatches 80
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                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 451
; TYPE: PRT
; ORGANISM: Human and
US-09-247-352-3
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US-09-247-352-3
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APPLICANT: Harris, Linda

APPLICANT: Horne, Barbara A.

APPLICANT: Bajorath, Jurgen

APPLICANT: Bajorath, Jurgen

APPLICANT: Huse, William D.

APPLICANT: Watkins, Jeffry D.

TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD

FILE REFERENCE: DB2a SEQUENCE

CURRENT APPLICATION NUMBER: US/09/247,352

CURRENT FILING DATE: 1999-02-10

EARLIER APPLICATION NUMBER: 09/026,291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro
APPLICANT: Siadak, Anthony W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09247352 Patent No. 6312693
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 276; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 14
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115
                                              138 SLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 LTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QL
                                                                                               65
                                                                                                                                                89
                                                                                                                                                                                                                                          30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD-
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GTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 174
                                                                                               KGRFAFSLETSANTAYLQISNLKNEDTATYFC-VRSGNGNYDLAYFA-----YWGQ 114
                                                                                                                                                                                                 LKKPGETVRISCKAS---GYAFTTTGMQWVQEMPGKG---LKWIGWINTHSGVPKYVEDF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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                                                                                                                              QGNFP-----LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQ 137
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                                                                                                                                                                                                                                                                                              Score 1264; DB 4;
Pred. No. 1.5e-94;
23; Mismatches 80;
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GENERAL INFORMATION:
APPLICANT: ARULIC, Alejandro A.
APPLICANT: Bladak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Harris, Linda
APPLICANT: Bajorath, Jurgen
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
FILE REFERENCE: DB2 SEQUENCE
CURRENT APPLICATION NUMBER: US/09/466,635
CURRENT FILING DATE: 1999-12-17
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US-09-466-635-3
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.4%; Score 1264; DB 4; Best Local Similarity 59.6%; Pred. No. 1.5e-94; Matches 276; Conservative 23; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09466635 Patent No. 6413514
                 269 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 328
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                                                                                                                                 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKT
                                                                                                                                                                                                 GTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 174
                                                                                                                                                                                                                                                                    KGRFAFSLETSANTAYLQISNLKNEDTATYFC-VRSGNGNYDLAYFA-----YWGQ 114
                                                                                                                                                                                                                                                                                                                                       LKKPGETVRISCKAS---GYAFTTTGMQWVQEMPGKG---LKWIGWINTHSGVPKYVEDF
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                                                                                                                                                                 -QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
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US-09-027-449-71
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 273; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/027,449

FILING DATE: 20-Feb-1998

CLASSIFICATION -435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/074,330

FILING DATE: 22-Jan-1998

PRIOR APPLICATION NUMBER: 60/074,330

FILING DATE: 22-Jan-1998

PRIOR APPLICATION NUMBER: 60/038,664

PILING DATE: 22-Jan-1998

PRIOR APPLICATION NUMBER: 60/038,664

PRIOR APPLICATION NUMBER: 60/038,664
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Patent No. 60251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650/252-9881
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
TOPOLOGY: Linear
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CITY: South San
STATE: Californi
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                                        VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                       SRDNSKNTAYLQMNSLRAEDTAVYYCARGDYR----
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  QDSG---
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                                                                                                                                                                                                                                                                                     52.3%; Score 1263.5; DB 3;
59.6%; Pred. No. 1.6e-94;
ative 26; Mismatches 86;
---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                         -----YNGDWFFDVWGQGTLVT
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US-09-026-985-71
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GENERAL INFORMATION:
                                                                                                                                            Matches 273;
                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CCLASSIFICATION:
                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acid
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                      H: 452 amino acids
Amino Acid
SRDNSKNTAYLOMNSLRAEDTAVYYCARGDYR-----YNGDWFFDVWGQGTLVT
                                W----DQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-LQGQSLTLT 142
                                                                  LVOPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFTL
                                                                                                        LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 451
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                       Linear
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                                                                                                                                                             52.3%; Score 1263.5; DB 59.6%; Pred. No. 1.6e-94;
                                                                                                                                                                                                                                                                                                                                                                                              34,659
                                                                                                                                          26;
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                                                                                                                                            Mismatches
                                                                                                                                                                              DB 3;
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RESULT 43
US-09-121-952A-71
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TELEPAX: 650/952-900.

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 71, Application US/09121952A
                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA: 60/074
APPLICATION UNMBER: 60/074
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075
APPLICATION NUMBER: 60/075
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080

COMPUTER READABLE FORM:

COMPUTER: 3.5 inch, 1.44 Mb fl

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Sapata, Gerardo A.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER (
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Genentech, Inc., Hs
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                            NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-Jul
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                                                                                                                     TELEPHONE:
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APPLICANT: Genentec
APPLICANT: Koumenis
APPLICANT: Leong, S
APPLICANT: Presta,
APPLICANT: Shahrokt
APPLICANT: Zapata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 646853
                                                                                                                                                                                                                                                                               APPLICANT: Presta, Leonard G.
APPLICANT: Shahroth, Zahra
APPLICANT: Shahroth, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER (
TITLE OF STOUENCES: 72
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
                                                                                           COMPUTER READABLE FORM:
MEDLIM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
                                                                                                                                                                                                                     STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09234340A
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Koumenis, Iphigenia
Leong, Steven R.
Presta, Leonard G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-234-340A-71
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 22-JAN-1998
PRIOR APPLICATION NUMBER: 60/075467
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                     354
                                                                                                     334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFTL
                       KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                   YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                              TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                    LESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QLEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                         SRDNSKNTAYLQMNSLRAEDTAVYYCARGDYR------YNGDWFFDVWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-LQGQSLTLT 142
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                     YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                        TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                                                                                                                                                                                                                                                                                                                     QDSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                   -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
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   451
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GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Imp
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049 RESULT 45 US-09-301-593-30 Sequence 30, Application US/09301593A Patent No. 6455677 Improved Producibility

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NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 271; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 472
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                  ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jard TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-U11-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               STREET: 1 .... STREET: A .... STREET: South San Fra CITY: California
                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Svoboda,
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                                                                                                                                                                                                                                                                                      Genentech, Inc.
                                                                                                                                                                                                                                                    Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08887352B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
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                                                                                                                                                                                                                                                                                                                                                                              Paula M. Jardieu,
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; OTHER INFORMATION: Heavy US-09-109-207C-18
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US-09-109-207C-18
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                                                                                                                                                      PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 18
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/09109207C
Patent No. 6172213
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acide
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554
                                                                                                                                                                                                                                                                             APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of In FILE REFERENCE: P1123R1
                                                                   NAME/KEY: Artificial LOCATION: 1-451
                                                                                                     FEATURE:
                                                                                                                    ORGANISM: Artificial
                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 SRDDSKNTFYLQMN-----SLRAEDTAVYYCARGSH-----YFG------HWHFAV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKYNPSVKGRITI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKTHTC-----PELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
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Pred. No. 2.2e-94;
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Query Match

52.3%;

Score 1262;

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Best Local Similarity

58.6%;

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; LENGTH: 451
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is co. 6194551
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US-09-282-505-2
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Best Local S
Matches 273
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Patent NO. 6194551
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
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SEQ ID NO 2
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WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                           QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
                                                            SRDDSKNTFYLOMN----SLRAEDTAVYYCARGSH---
                                                                                          DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
                                                                                                                         LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKYNPSVKGRITI
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                                                                                                                                                                                    Score 1262; DI
Pred. No. 2.2e
25; Mismatches
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5; Mismatches 78;
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                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                     Length 451;
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US-09-054-255-2
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APPLICANT: Esohe Ekinaduese Idusogie et a.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.3%;
Best Local Similarity 58.6%;
Matches 273; Conservative 29
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Patent No. 6242195
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TYPE: PRT
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GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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Pred. No. 2.2e-94;
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Gaps

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172

224

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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Prest;
TITLE OF INVENTION: Improved Anti-IgE Antibo;
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005;
CURRENT FILING DATE: 1999-04-21;
EARLIER APPLICATION NUMBER: US 08/887,352;
EARLIER FILING DATE: 1997-07-02;
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 18
LENGTH: 451
                                                                                                     RESULT 51
US-09-282-846-2
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US-09-296-005-18
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              Sequence 2, Application US/09282846
Patent No. 6528624
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
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Best Local S
Matches 273
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Patent No. 6290957
 FILE REFERENCE:
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ORGANISM: Artificial
FEATURE:
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d Anti-IgE Antibodies
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Pred. No. 2.2e-94
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of Improving Polypeptides
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/680,145
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 09/282,505
PRIOR FILING DATE: 1999-03-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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US-09-282-846-2
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ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INFORMATION: Sequence is completely synthesized
Patent No. 6528624
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CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09680145 Patent No. 6538124
Patent No.
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Matches 273;
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              NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INFORMATION: Sequence is completely
                                                                                                     LENGTH: 451
TYPE: PRT
                                                                   FEATURE:
                                                                                 ORGANISM: Artificial
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58.6%;
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Pred. No. 2.2e-94;
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TITLE OF INVENTION: Improved Anti-IgE Antibodies (as FILE REFERENCE: P1123C2US CURRENT APPLICATION NUMBER: US/09/920,171 CURRENT FILING DATE: 2001-08-01 PRIOR APPLICATION NUMBER: US 08/887,352 PRIOR FILING DATE: 1997-07-02 PRIOR APPLICATION NUMBER: US 09/296,005 PRIOR FILING DATE: 1999-04-21 NUMBER OF SEQ ID NOS: 44 SEQ ID NOS: 44
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                                                                                                                                        OTHER INFORMATION: Heavy chain sequence derived US-09-920-171-18
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                                                                      Query Match
Best Local S
Matches 273
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Best Local (
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                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                 LENGTH: 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                 30 LGKKGDTVELTCTASQ----KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 SRDDSKNTFYLOMN-----SLRAEDTAVYYCARGSH-----YFG-----HWHFAV 110
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                                                                                        Similarity
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LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKYNPSVKGRITI
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                                                                                      Score 1262;
Pred. No. 2.
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                                                                      Mismatches
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                                                                                      DB 4;
2.2e-94;
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                                                                                                     Length 451;
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RESULT 54
US-09-049-672A-8
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Sequence 8, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter D
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Weil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Wariah R.
APPLICANT: Baughn, Wariah R.
APPLICANT: HOMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
                                                                                                                NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
                                                           TELEFAX:
                                                                           TELEPHONE:
                                                                                                                                                                                               FILING DATE
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                                                           650-845-0555
650-845-4166
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RESULT 55

US-09-499-846-12

Sequence 12, Application US/09499846

Patent No. 6656728

GENERAL INFORMATION:

APPLICANT: Kavanaugh et al.

TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS

FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846

CURRENT FILING DATE: 2000-02-07

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 12

LENGTH: 488

TYPE: PAT

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
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Query Match
Best Local Similarity
Matches 272; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 TYICEVEDQKEEVQLLVFGLTANSDTHL-----LQGQSLTLTLESPPGSSPSVQCRSPRG 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KNSNQI----KILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSD 105
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52.2%; Score 1261; DB 4; Length 488; ilarity 57.9%; Pred. No. 2.9e-94; Conservative 30; Mismatches 88; Indels 8
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US-08-466-151-8 US-08-466-151-8 Sequence 8, Application US/08466151 Patent No. 6037453 GENERAL INFORMATION: APPLICANT: Jacadiew, Paula M. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Immunoglobulin Variants NUMBER OF SEQUENCES: 65 UNDMERE OF SEQUENCES: 65 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA May CITY: South San Francisco STATE: California COUNTRY: USA ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: WinPatin (Genentech) CURRENT APPLICATION NUMBER: US/08/466,151 FILING DATE: 15-MAR-1995 APPLICATION NUMBER: 08/466613 FILING DATE: 15-MAR-1995 APPLICATION NUMBER: 08/466163 FILING DATE: 15-MAR-1995 PRIOR APPLICATION NUMBER: 08/466163 FILING DATE: 26-JAN-1994 PRIOR APPLICATION NUMBER: 07/474768 FILING DATE: 17-MUG-1991 APPLICATION NUMBER: 07/44768 FILING DATE: 11-AUG-1991 APPLICATION NUMBER: 07/744768 FILING DATE: 11-AUG-1991 ATTORNEY/AGENT INFORMATION:	QY 15 CLALLPAATQCNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIKILGNQGSFLTKGP 1

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Sequence 8, Application US/08466163B

Patent No. 6329509

GENERAL INFORMATION:

APPLICANT: Jarddeu, Paula M.

APPLICANT: Presta, Leonard G.

APPLICANT: Presta, Leonard G.

FILE REFERENCE: P0718P2C1D1

CURRENT APPLICATION NUMBER: US/08/466,163B

CURRENT FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR FILING DATE: 1992-05-07

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR APPLICATION NUMBER: US 07/744,768
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                                     NUMBER OF SEQ ID SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.2%; Score 1259; DB 3; Best Local Similarity 58.9%; Pred. No. 3.8e-94; Matches 271; Conservative 26; Mismatches 87;
LENGTH:
TYPE: PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
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; FEATURE:
; OTHER INFORMATION:
US-09-802-096-8
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR PRICATION NUMBER: US 08/185,899
PRIOR PRICATION NUMBER: PCT/US92/06860
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR PILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PRILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PRILING DATE: 1991-08-14
PRIOR PRILING DATE: 1991-08-14
PRIOR PRILING DATE: 1991-08-14
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                                                        SEQ ID NO 8
LENGTH: 453
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application Patent No. 6685939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 271;
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended FILE REFERENCE: P0718P2C3US
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jardieu, APPLICANT: Presta,
                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: humanized maell, version 1 heavy chain
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Pred. No. 3.8e-94
6; Mismatches 8
                       version
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                     heavy
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Query Match

Score 1259;

BB

4

Length 453;

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RESULT 59
US-08-378-939-10
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                                             APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6640
                TELEFAX: (202) 783-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THARTEENTH ST. N.W.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----QL
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                                   (202)
                                 783-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 60
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APPLICANT: Anderson, Da:
TITLE OF INVENTION: "MOI
TITLE OF INVENTION: PHAI
TITLE OF INVENTION: PHAI
TITLE OF INVENTION: PHAI
TITLE OF INVENTION: IMM
RUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08487550
Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 258; Conserv
                ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                         ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                       STREET: 699 Prin
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                     COUNTRY: UI
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 PSVQCRSPRGKNIQGG-----KTLSVS------QLELQDSG----
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Conservative 17
                                                                                                                                                                                                                                                                                                                                                            699 Prince
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IVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS IVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND
                                                                                                                                                                                                                                                                                                        USA
703-836-2021
                                                                                                                                                                                                                                                                                                                                                                            BURNS, DOANE,
                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                            Street
                                                                                                                                                               US/08/487,550
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Pred. No. 4.1e-94;
                                                       012712-131
                                                                                                                                                                                                                                                                                                                                                                              SWECKER & MATHIS
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; Sequence 8, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBOD
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 61
US-09-526-098-8
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                                                                                                                                                                  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.2%; Score 1259; DB 3; Best Local Similarity 66.9%; Pred. No. 4.1e-94; Matches 259; Conservative 12; Mismatches 56;
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383
FILING DATE:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND
                         US 08/487,550
                                                                      09/383,916
                                                                                                                                                             US/09/526,098
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PATENT NO. 6656728

GENERAL INFORMATION:
APPLICANT: KAVANAUSH Et al.
TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU:
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
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                                                        Query Match
Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.2%; Score 1259; DB 4; Best Local Similarity 66.9%; Pred. No. 4.1e-94; Matches 259; Conservative 12; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09499846
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 0127

TELECOMMUNICATION INFORMATION:

TELECHONE: 703-836-6620
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QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69 :| :| | | | : : : | | | : :
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                                                            Conservative
                                                        52.1%; Score 1258.5;
57.1%; Pred. No. 4.86
tive 30; Mismatches
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                                                                             4.8e-94;
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                                                                                               DB 4;
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TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 525
TYPE: PAT
ORGANISM: Homo sapiens
US-09-499-846-8
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US-09-499-846-8
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Patent No. 6656728
GENERAL INFORMATION:
APPLICANT: Kavanaugh et al.
                                                                                                                                                                                                                                                                                                    Query Match 52.1%; Score 1258.5; DB Best Local Similarity 57.1%; Pred. No. 5.1e-94; Matches 274; Conservative 30; Mismatches 85
                                204
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-----APEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
|||||||||||||
EGSGSPGLQEPKSCDKTHTCPPCPAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 344
                                                                                          --OGGKTLSVSQLELQDSGTWTC----
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                                                              TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
                                                                                                                      AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT
                                                                                                                                                    FGLTANSDTHLLQGQSLTLTLESPP------
                                                                                                                                                                                  TWSIIMDSVVPS----
                                                                                                                                                                                                              TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                                                                                                                            KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGSGSPGLQEPKSCDKTHTCPPCPAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
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                                                                                                                                                                               ---DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 167
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                                                                                          ----TVLQNQKKVEFKIDIVPCP---
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                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                   GSS----PSVQCRSPRGKNI 163
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US-08-887-352B-16
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 272; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRITATION INFORMATION:
APPLICATION DATA:
APPLICATION UMMBER: US/08/887,352B
PILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPAN: 650/225-1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Henry
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 451 amino acids TYPE; Amino Acid TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
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CITY: South San
STATE: Californi
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                                      WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                                          QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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Pred. No. 5.5e-94;
5; Mismatches 79
-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
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                                                                                                                                                                                                                                                                                                           Length 451;
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US-08-466-151-65
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/466
FILING DATE: 06-7un-1995
APPLICATION NUMBER: 08/405
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185
FILING DATE: 26-CAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acid
                                                                                                                                                                                            APPLICATION NUMBER: 07/74
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                              NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: PO
                   LENGTH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/466,151 FILING DATE:
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TOPOLOGY:
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Linear
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US-09-109-207C-14
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 14
LENGTH: 451
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Best Local
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                                                                  -09-109-207C-14
                                                                                                                                                                                                                               FEATURE:
NAME/KEY: Arrificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial
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                                                                                                                                                                                 Similarity
     QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---
                                     SRDDSKNTFYLOMN-----SLRAEDTAVYYCARGSH-----YFG-----
                                                                  DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH----LL
                                                                                                   LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI
                                                                                                                                LGKKGDTVELTCTASO----KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN------
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                                                                                                                                                                52.1%; Score 1257; DB 3;
58.4%; Pred. No. 5.5e-94;
7ative 25; Mismatches 79
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58.4%;
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nes 79;
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                                                                                                                                                                                                 Length 451;
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     -KTLSVS------
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                                     -HWHFAV
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Patent No. 6172213

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M.

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Met

FILE REFERENCE: P1123R1

CURRENT APPLICATION NUMBER: US/09/109,207C

CURRENT FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44
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; OTHER INFORMATION: Heavy chain sequence
US-09-109-207C-16
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US-09-109-207C-16
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LENGTH: 451
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: Artificial
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                                                                   DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
                                                                                                                                                                                                                  QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
GVEVHNAKTKPREEGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                               VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
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                                                    DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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Pred. No. 5.
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hes 79;
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FEATURE:
INAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14
         RESULT 70
US-09-296-005-16
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Best Local S
Matches 272
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT PFLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
ARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 451
Type: New Par
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                                                                                                                                                                  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
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                                                                             DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                 GOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
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Sequence 14, Application US/09920171

Patent No. 6682735

GENERAL INFORMATION

APPLICANT: Lowman, Henry B.

APPLICANT: Presta, Leonard G.

APPLICANT: Dardieu, Paula M.

APPLICANT: Lowe, John

TITLE OF INVENTION: Improved Anti-IgE Antibodies (as FILE REFERENCE: P1123C2US)

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: US/09/920,171

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: US 08/887,352

PRIOR FILING DATE: 1997-07-02
                                                                                                                                                                                                                                        RESULT 71
US-09-920-171-14
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; FEATURE:
, NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy
US-09-296-005-16
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Best Local Similarity
Matches 272; Conserv
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SEQ ID NO 16
LENGTH: 451
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Patent No. 6290957
GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving PFILE REFERENCE: P1123Clr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial
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DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                          DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                       GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                               DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN------
                                                                                GOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                    GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                         VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
                                                                                                                                                                                                                                                                                                                                                              ----QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----
                                                                                                                                                                                                                                            DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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Pred. No. 5.5e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SLRAEDTAVYYCARGSH-----YFG-----HWHFAV 110
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US-09-920-171-16
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; OTHER INFORMATION: Heavy chain sequence US-09-920-171-16
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                                                                                                      PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Applicate Patent No. 6682735
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 199-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                               APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Heavy chain sequence derived from MAE11-09-920-171-14
                                ORGANISM: Artificial Sequence FEATURE:
                                                                      LENGTH: 451
TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRDDSKNTFYLQMN-----SLRAEDTAVYYCARGSH----YFG-----HWHFAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
                                                                                                                                                                                                                                                                                                                                                                                                     Application
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                   derived
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                   from MAE11
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Sequence 8, Application US/087934:
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTI
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 73
US-08-793-450-8
                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08793450
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                                                                                                                                                                                                                                                                                                                                     USA
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24,618
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Query Match
Best Local Similarity
Matches 272; Conserv 345 285 266 171 173 111 405 386 326 71 SRDDSKNTFYLOMN-----SLRAEDTAVYYCARGSH----YFG-----HWHFAV 110 78 11 30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN------GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325 DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385 VHTFPAVLQSSGLYSLSSVVTVPSSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210 Conservative 52.1%; Score 1257; DB 4; Length 451; 58.4%; Pred. No. 5.5e-94; tive 25; Mismatches 79; Indels 9 450 Gaps 344 265 284 224 12;

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GENERAL INFORMATION:

APPLICANT: Park, John E.

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Leger, Olivier

APPLICANT: Leger, Olivier

APPLICANT: Saldanha, Jose W.

APPLICANT: Saldanha, Jose W.

APPLICANT: Rettig, Wolfgang J.

TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility

FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A

CURRENT FILING DATE: 1999-04-29

EARLIER APPLICATION NUMBER: EP 98107925.4

EARLIER FILING DATE: 1998-04-30

EARLIER FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 108

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 43

TENCTH. 472
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 74
US-09-301-593-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 660
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/09301593A Patent No. 6455677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.1%; Score 1257; DB 4; Best Local Similarity 59.0%; Pred. No. 5.9e-94; Matches 268; Conservative 25; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471
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APPLICANT: Pai, Emil F.
APPLICANT: Klein, Michel H.
APPLICANT: Klein, Michel H.
APPLICANT: Klein, Michel H.
APPLICANT: Chong, Pele
APPLICANT: Pedyczak, Arthur
TITLE OF INVENTION: Fab'-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
FILE REFERENCE: 1038-926 MIS:jb
CURRENT APPLICATION NUMBER: US/09/289,942A
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEG ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 7
LENGTH: 462
TYPE: PRT
ORGANICM: Human immunodeficiency virus type 1
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US-09-289-942A-7
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                                                                                                                                                                                                               US-09-289-942A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09289942A Patent No. 6482928 GENERAL INFORMATION:
                                                                                                                                     Matches
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                                                                                                                                                       Match 52.0%;
Local Similarity 66.2%;
138
                                 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
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                                                                                                                                        258;
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                                                                                                   94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-TANSDTHLLQ--GQSLTLTLESPPGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GINPNNGIPNYNQKFKGRATLTVGKSASTAYMELSSLRSEDTAVYYC-----ARRRIA 121
                             PSVQCRSPRGKNIQGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGY----DEGHAMDYWGQGTLVTVSSST-KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIG--
PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 197
                                                                    LVMTRVSPVDTATYFC----AHRRGPTTLFGVPIARGPVNAMDVWGQGITVTISSASTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.1%; Score 1256.5; DB 4; ilarity 56.9%; Pred. No. 6.5e-94; Conservative 38; Mismatches 86;
                                                                                                                                        18;
                                                                                                                                     Score 1255; DB 4;
Pred. No. 8.3e-94;
8; Mismatches 52;
                                 --KTLSVS----
                                                                                                                                                                    Length 462;
                                                                                                                                        Indels
                               ----QLELQDSG----
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                                                                                                                                        62;
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                                                                                                                                     Gaps
                                 180
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GENERAL INFORMATION:
APPLICANT: BASBY, CAROL D.
APPLICANT: BLANK, GREG S.
ITITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1D2
CURRENT APPLICATION UNMBER: US/09/679,397
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR APPLICATION NUMBER: US 09/304,465
PRIOR APPLICATION NUMBER: US 09/304,465
PRIOR FILING DATE: 1998-05-03
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 449
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US-09-679-397-2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.0%; Score 1254.5; DB 4; Length Best Local Similarity 57.8%; Pred. No. 8.8e-94; Matches 268; Conservative 30; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Sequence is synthesized 09-679-397-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342
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 286
                                  268
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                  EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                       THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                         TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                            --QLELQDSG--------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
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EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                   THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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CURRENT APPLICATION NUMBER: US/09/680,148
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
PRIOR PRIOR PRIOR NUMBER: US 09/304,465
PRIOR PILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
LENGTH: 449
TYPE: PRT
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US-09-680-148-2
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Best Local (
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APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Sequence is synthesized
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                                                                                                                                                                                       268
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                                                                                                                                                                                                                                                THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                       SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                         PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                       EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
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                                                                                                                                                  EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                            THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
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FILE REFERENCE: F124IR1
CURRENT APPLICATION NUMBER: US/09/304,465A
CURRENT FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 449
TYPE: PRT
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US-08-487-550-4
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                                                              Sequence 4, Application US/08487550
Patent No. 6113998
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND TITLE OF INVENTION: IMMUNOSUPPRESANTS"
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Best Local Similarity
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OTHER INFORMATION: Sequence
Patent No. 6489447
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PATENT NO. 6489447
GENERAL INFORMATION:
APPLICANT: BASEY, CAROL D.
APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
STREET: 699 Prince Street
                                                        NUMBER OF SEQUENCES:
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57.8%;
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RESULT 80
US-09-526-098-4
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Best Local Similarity 59.2%;
Matches 270; Conservative 20
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4
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LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: TESKII, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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ZIP: 22314
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STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                            LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPFVLDSDGSFFLYSKL
                                                                                                                                                                        LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 395
                                                                                                                                                                                                                                       PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----QLELQD
                                                                       TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Sequence 4, Application US/09526098
PATCHI NO. 6492134
GENERAL INFORMATION:
APPLICANT: ANGERSON, Darrell R.
APPLICANT: ANGERSON, DARRELL R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED EX

FORMS THEREOF,

379

319

259 216

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PRIOR APPLICATION NUMBER: 09/383, y10
APPLICATION NUMBER: 09/383, y10
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teakin, Robin L,
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-13
TELECOMMUNICATION 1076-6620
TELECOMMUNICATION: 703-836-6620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 699 Princ
CITY: Alexandria
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                                                                                 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 395
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                         LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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                     431
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 951
TYPE: PRT
           Sequence 7, Application US/08472888A
Patent No. 6613746
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Walz, Gerd
TITLE OF INVENTION: AGP-ANTIBODY FURTITIES OF INVENTION: AND RELATED MO
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US-09-313-942-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                   932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520 SKGPTVRTKKVGKNEAVLEWDO--LPVDVONGFIRNYTIFYRTIIGNETAVNVDSSHTEY 577
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                                                                                                                                                                                                                                                           MHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                   LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412
                                                                                                                                                                                                                                                                                                                                                                                                           VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKP 232
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                                                                                                                                                                                                                                                                                                           LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
                                                                                                                                                                                                                                   MHEALHNHYTOKSLSLSPG
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AGP-ANTIBODY FUSION PROTEINS AND RELATED MOLECULES AND MET 9
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Pred. No. 3.4e-92;
33; Mismatches 66; Indels 85;
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                     AND METHODS
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RESULT 83
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Sequence 9, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
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Best Local Similarity 74.1
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION UMBER: US/08/472,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/618,314
PILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/258001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 442 amino acids
TYPE: amino acid
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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STREET: 176 Fe
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
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TELEFAX: 617-428-7045
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                                                                                                                                                                                             SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                        RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                     QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
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RESULT 84
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acide
TYPE: amino acid
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 0076
REFERENCE/DOCKET NUMBER: 0076
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lir
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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TELEFAX: 617/542-8906
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ZIP: 02210-2804
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                                                                SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441
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Pred. No. 1.9e-92;
2; Mismatches 26
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Sequence 54, Application US/09746359A Patent No. 6610286 GENERAL INFORMATION:

APPLICANT:

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PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 3.
SEQ ID NO 54
LENGTH: 547
TYPE: PRT
ORGANISM: Homo sapiens
              GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
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                                                                                                                                        Sequence 53, Application Patent No. 6610286
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
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APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 51.3%; Score 1238; DB 4; Length 547;
Local Similarity 58.8%; Pred. No. 2.5e-92;
nes 276; Conservative 23; Mismatches 72; Indels 9
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Xu, Wenfeng
Madden, Karen L.
Kelly, James D.
Sprecher, Cindy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLWDQ--GNFPLIIKNLKIEDSDTYICEVED-----QKEEVQLLVFGLTANSDTHL 133
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Blumberg, Hal
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Kelly, James D.
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                                                                                                                                                             US/09746359A
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                                                                                                                                  Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 53
LENGTH: 571
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Best Local Similarity
Matches 276; Conserv
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APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/746,359A CURRENT FILING DATE: 2001-05-21 PRIOR APPLICATION NUMBER: 60/171,969 PRIOR FILING DATE: 1999-12-23 PRIOR APPLICATION NUMBER: 60/213,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                          NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
  COUNTRY:
                                                                                                                                                                                                                                                                                                                                           522
                                                                                                                                                                                                                                                                                                                                                                                383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 LQGQSLTLTLESPPGSS--PSVQCRSPRGKNIQGG------KTLSVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 EVALTTDEKSISVVLTAPEK-----WKRNPEDLPVSMQQIYSNLKYNVSVLNTKSN--- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 KVVLGKKGDTVELTCTASQKKSIQFHWK-NSNQIKILGNQ-GSFLTKGPSKLNDRADSRR 84
                                                                                                                                                                                                                                                                                                                                                                LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTWSQCVTNHTLVLTWL--EPNTLYCVHVESFVPGPPRRAQPSEKQC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLWDQ--GNFPLIIKNLKIEDSDTYICEVED-----QKEEVQLLVFGLTANSDTHL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                            KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ARTLKDQSSEASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
                                                                                                                                                                                                                                                                                                                                           LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                        KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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Pred. No. 2.7e-92;
                                                            Blvd
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461

401

341

Length Indels

571; ,86

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RESULT 87
US-08-457-918-7
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
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Best Local Similarity
Matches 249; Conserv
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/10
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: 07/942777
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415/952-9881
                                                                                                                                                                                                                                 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 KTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 266
                                                                                                                                                                                            326 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 370
                                                                                                                                                                                                                                                                                                                                                    206 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 GQSLTTTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 GLGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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                                                                                                                                                                                                                  GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                       QPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                                                                                                                                                                                                                                                               QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 386
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72.2%;
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Pred. No. 1.9e-92;
9; Mismatches 32; Indels 55;
                                                                                                                                                                                                                                 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/936190
PRILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA: 07/842777
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA: 07/250785
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA: 07/104329
PRIOR APPLICATION DATA: 07/104329
APPLICATION NUMBER: 07/104329
APPLICATION NUMBER: 08/575
ATTORNEY/AGENT INFORMATION:
NAME: KUBLING: Jeffrey S.
REGISTRATION NUMBER: 36,575
REGISTRATION NUMBER: 36,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/2
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Adheson Variants NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/457,918 FILING DATE: 1-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bru
                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 51.2%;
Local Similarity 72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                                                                                                                                                                                                                                                                                     173 ---QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211
                                                                                                                                                                                                                                                                                                                                                                              136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------
                                                                                                                                                                                                                                                                92 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD
                                   VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                       KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                          KTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                                                                                                                                         GLGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 91
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                              VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.9e-92;
9; Mismatches 32; Indels
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326

GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 370

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APPLICANT: LOBB, ROY R.

APPLICANT: Burkly, Linda C.

TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DIS

FILE REFERENCE: 10274-004003

CURRENT APPLICATION NUMBER: US/09/157,452B

CURRENT FILING DATE: 1998-09-21

PRIOR APPLICATION NUMBER: US 08/950,660

PRIOR FILING DATE: 1997-10-15

PRIOR APPLICATION NUMBER: US 08/373,857

PRIOR APPLICATION NUMBER: US 08/373,857

PRIOR APPLICATION NUMBER: US 08/284,603

PRIOR APPLICATION NUMBER: US 08/284,603

PRIOR FILING DATE: 1995-01-18

PRIOR APPLICATION NUMBER: US 08/284,603

PRIOR FILING DATE: 1993-02-02

PRIOR APPLICATION NUMBER: US 07/835,139

PRIOR APPLICATION NUMBER: US 07/835,139

PRIOR APPLICATION NUMBER: US 07/835,139

PRIOR FILING DATE: 1993-02-02
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US-09-157-452B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.3
---- 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens -09-157-452B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 446
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  395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LLVFGLTANSDTHLLQGQSLTLTLESPP---GSSPSVQCRSP------RGKNI 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 LALLPAATQGNKV------VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILG---NQ 65
                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                               EPXSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                            PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                          ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
                                                                                                                                                                         NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                             MKSQEFLEDADRKSLETKSLEVTFTPVIEDIG----KVLVCRAKLHIDEMDSVPTVRQAV
                                                                                                                                                                                                                                                                                                                                                                                     QGG-----KTLSVSQLE-----LQDSGTWTCTVLQNQKKVEF-KIDIVPC--PAP 205
                                                                                                                                                                                                                                                                                                                                                                                                                               VEIYSFPKDPEIHL------SGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTSTLTMNP---------VSFGNEHSYLCTATCESRKLEKGIQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G--SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV--EDQKEE--VQ
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                    ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                           KELQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.1%; Score 1234.5; DB 4; Length 446; 57.3%; Pred. No. 3.6e-92; ative 36; Mismatches 70; Indels 95;
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RESULT 89 US-09-590-656-2 ; Sequence 2, Application US/09590656

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US-09-733-764-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cerretti, Douglas P.
APPLICANT: Bozges, Luis G.
APPLICANT: Bozges, Luis G.
APPLICANT: FARBLOW, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/137,889
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/733,764
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/590,656
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
APPLICANT: Borges, Luis G.
APPLICANT: Fanslow, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                        Query Match
Best Local Similarity
Matches 236; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09733764 Patent No. 6521424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                        LENGTH: 704
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mes 236; Conserv
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 418
                                    178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 DSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGEPKSC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 DSGTWTCTVLQNQKKVE--FKIDIVPCPAP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQPREPQYYTLPBSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
 DSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGEPKSC
                                   DSGTWTCTVLQNQKKVE--FKIDIVPCPAP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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                                                                         Conservative
                                                                                         51.0%;
82.5%;
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Pred. No. 1.1e
4; Mismatches
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                                                                                         Score 1232; DB 4;
Pred. No. 1.1e-91;
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1e-91;
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                                                                         Indels
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477
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US-08-461-968A-5
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                                                                                                                                 Query Match 50.8%; Score 1226; DB 1; Best Local Similarity 73.5%; Pred. No. 1.8e-91; Matches 244; Conservative 12; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08461968A Patent No. 5801044
GENERAL INFORMATION:
APPLICANT: Seed et al., Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-005/MS-00S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/08/461,968A
FILING DATE: 05-UN-1995
                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-461-968A-5
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/618,314
FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/06701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                           TELEX: 200154:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Seed et al., Brian
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 225 F
CITY: Boston
STATE: MA
136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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                                                           122 GOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181
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                                                                                                                                                                                                                                                   ss: not relevant
linear
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                                                                                                 ----KTLSVS-----
                                                                                                                                                                         Length 442;
                                                                                                                                   Indels 48;
                                                                                                                                   Gaps
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RESULT 93
PCT-US96-10043-11
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                                                                                              Matches
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION UMBER: US 60/000
APPLICATION NUMBER: US 60/000
EILING DATE: 14-UN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 0078
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: P-SELECTIN 1 TITLE OF INVENTION: AND METHODS NUMBER OF SEQUENCES: 14
                                                                                                                                                                                      TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The General Hospital Corporation TITLE OF INVENTION: P-SELECTIN LIGANDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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                                                       99 LKIEDSDTYIC -- EVEDOKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQC-
                                                                                                                                                                                                                                          amino acid
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                     LILROTKTYMLAFOVNDEKN-----WGLSVYADKPETTKEQLGEFYE-----ALDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
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                                                                                              Conservative
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                                                                                                         50.7%; Score 1224; DB 5; 72.3%; Pred. No. 2.5e-91;
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                                                                                              Mismatches
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                                                                                                                            Length 437;
                                                                                            Indels
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APPLICANT: Bark, John E.

APPLICANT: Barnberger, Uwe
APPLICANT: Barnberger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Prod
FILE REFERENCE: 0652-1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 330
TYPE: PRT
GRGANISM: Homo sapiens
US-09-301-593-22
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.6
Best Local Similarity 73.9
Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 645567
                                      240
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   402
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                                                                                                                                                                                                                                                             SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 119
                                                                                                         NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 330
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                                                                                                                                NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
                                                                                                                                                                                                                                                                                                 -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
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   WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                             ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
                                                                                                                                                                                      GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 179
                                                                                                                                                                                                                                                                                                                                    PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                        EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 1221.5; DB Pred. No. 2.7e-919; Mismatches 2
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PCT-US95-03866-12
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US-09-313-942-8
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                                                                                                                                                                                    Sequence 12, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09313942
PATENT NO. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8
LENGTH: 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.6%; Score 1221; DB 4; Length 592; Best Local Similarity 80.5%; Pred. No. 6.7e-91; Matches 236; Conservative 10; Mismatches 22; Indels 2
COUNTRY: United States of ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatibl
OPERATING SYSTEM: PC-DOS/M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/101,858 PRIOR FILING DATE: 1998-09-25
                                                                                                                 STATE: New York
                                                                                                                                                       STREET:
                                                                                                                                                                          ADDRESSEE: Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 SPSVQCRSPRGKNIQGGKTLSVS-----QLELQDSGTWTCTVLQNQKKVEFKIDIVPCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKT
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                                                                                                                                                     1251 Avenue of the Americas
   PC-DOS/MS-DOS
                                                                                               of America
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                                                                                                             NUMBER OF SEQUENCES: 3
                                     STREET: 1251 A:
CITY: New York
STATE: New Yor
COUNTRY: UI
                                                           ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
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RESULT 97
PCT-US95-03866-14
Sequence 14. Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states exc
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: FIT-3/FLK-2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/03866 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 08/220,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CY
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                               MHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVA-----SETSDCV 164
                                                                                                                                                                                                                                           MHEALHNHYTQKSLSLSPG
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                                                                                    (all states except
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New York Y: United

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RESULT 98
US-09-180-100-11
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TELECOMMUNICATION INFORMATION:
TELESHOUNE 212-596-9000
TELESHAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS;
LENGTH: 424 amino acids
                                                                                                                                       Sequence 11, Application US/09180100 Patent No. 6306395
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 253; Conserv
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
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FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                             VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSSTLSPEKDSRVSVTKPFMLPPVAADPEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLLQGQSLTLTLESPPGSSPSVQCRSPR-----GKNIQGGKTLSVSQLELQDSGTWTCT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDSLTDLLDKFSNISEGLSNYSIIDKLVNIVD-DLVECVKENSSKDLK-------
                                                                                                                                                                                                                                                                     MHEALHNHYTQKSLSLSPG
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Sequence 22, Application US/09180100
PAtent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, Shigekazu
TITLE OF INVENTION: NOVEL FAB ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT TILING DATE: 1998-11-02
EARLIER APPLICATION UMBER: PCT/JP97/01502
EARLIER APPLICATION DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-180-100-22
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 22
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SOFTWARE: PatentIn Ver.
SEQ ID NO 11
                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                               SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
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                                                                                                                                                                                             CTLTSNTKCKE-----EGSRSNEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
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             PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
                                                                                 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
                                                                                                                              SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
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                                                            LNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFY
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Pred. No. 1e-90;
2; Mismatches 10;
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Pred. No. 1.1e-90;
2; Mismatches 10;
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Sequence 8, Application US/0933593A

Patent No. 6313269

GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: DEEN, KEITH C.
APPLICANT: TOUNG, PETER R.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TRONEH, ALEMSBEED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILLE OF INVENTION: TR6
FILLE OF INVENTION NUMBER: US/09/333,593A
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/913,684
PRIOR APPLICATION NUMBER: 08/913,684
PRIOR APPLICATION NUMBER: 08/913,684
PRIOR APPLICATION NUMBER: 08/913,094
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOPTWARE: FastSEQ for Windows Version 3.0
LENGTH: 424
TYPE: PRT
ORGANISM: HOMO SAPIENS
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                                                                          349 SLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 408
                                                                                                                                                                                                                                    229 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 NHYTOKSLSLSPG 431
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363 NHYTOKSLSLSPG 375
                                                                                                                                                                                                                                                                                                                                                                                                  168 GDCTPWSDIECVHKESGRSIEGR-----GTEPKSADKTHTCPPCPAPELLGGPSVFLF
                                                                                                                                                                                                                                                                                                                                                                                                                         177 QDSGTWT----CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 EVELSPCTTTRNT---VCQCEEGTFREEDSPEMCRKCRTGCPRG------MVKV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
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